

From: Mertz, Prema
Sent: Tuesday, December 20, 2005 12:42 PM
To: STIC-Biotech/ChemLib
Subject: 10/789,251

Please search SEQ ID NO2 with protein databases.

Please search SEQ ID NO:26 with DNA databases.

Please search SEQ ID NO:2, 26 with US PG PUB databases.

Thanks.

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Searcher: _____
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Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6				
Run on:	December 24, 2005, 10:22:43 ; Search time 16 Seconds				
Title:	US-10-789-251-2				
Perfect score:	910				
Sequence:	1 MKASSLAFSFLSAAFLYLWTT. AVVKALGELDILLOWMEETE 176				
Scoring table:	BLOSUM62				
	Gapop 11.0 , Gapext 0.5				
Searched:	283416 seqs, 96216763 residues				
Total number of hits satisfying chosen parameters:	283416				
Minimum DB seq length:	0				
Maximum DB seq length:	200000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 100%				
	Listing first 45 summaries				
Database :	PIR 80:*				
1:	pir1:*				
2:	pir2:*				
3:	pir3:*				
4:	pir4:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query	Match Length	DB ID	Description
1	156.5	17.2	178	2 A38580	interleukin-10 precursor - human
2	155	17.0	170	1 Q8BZ2	BCRFL protein - hu
3	155	17.0	175	2 I45591	interleukin 10 - p
4	147.5	16.2	179	2 A49558	interleukin 10 hom
5	144	15.8	178	2 A34853	interleukin-10 pre
6	136	14.9	178	2 JN0725	interleukin-10 pre
7	94.5	10.4	567	2 A45977	rab geranylgeranyl
8	94.5	10.4	809	2 S64594	probable beta-adap
9	93.5	10.3	140	2 F83128	probable transcript
10	81.5	9.0	646	2 T33346	hypothetical prote
11	81	8.9	1062	2 S46367	protein kinase CDC
12	80	8.8	2 T19295		hypothetical prote
13	76.5	8.4	502	2 AD1160	hypothetical prote
14	76.5	8.4	553	2 B9053	2-isopropylmalate
15	76.5	8.4	523	2 S6826	probable membrane
16	76	8.4	523	2 S6826	hypothetical prote
17	76	8.4	917	2 T21870	probable syncrocy
18	75	8.2	276	2 B71517	ATP-dependent RNA
19	75	8.2	726	2 T48023	probable pre-mRNA
20	75	8.2	729	2 H84912	hypothetical prote
21	74.5	8.2	121	2 E83640	probable exonuclease
22	74.5	8.2	1047	2 D71302	ATP-dependent DNA
23	74	8.1	682	1 H69879	UDP-N-acetylglucosamine
24	73.5	8.1	449	2 B71917	sensory box histid
25	73.5	8.1	653	2 D87602	membrane export pr
26	73.5	8.1	729	2 F97321	late protein, 100k
27	73.5	8.1	782	2 S33945	hypothetical prote
28	73.5	8.1	794	2 A98211	hypothetical prote
29	8.1		794	2 C86057	hypothetical prote

30	73	8.0	471	2 B38637	Ras inhibitor (clo
31	73	8.0	563	2 D90331	excinuclease ABC 8
32	73	8.0	614	2 E83880	hypothetical prote
33	73	8.0	1008	2 D84434	probable receptor
34	72.5	8.0	261	2 H98113	transcription repr
35	72.5	8.0	388	2 T06641	hypothetical prote
36	72.5	8.0	409	2 A54750	TNF receptor assoc
37	72.5	8.0	447	2 T20552	hypothetical prote
38	72.5	8.0	481	2 S39682	YML protein - Bac
39	72.5	8.0	1101	2 T33153	hypothetical prote
40	72.5	8.0	2182	2 T28634	variant-specific s
41	72.5	8.0	2581	2 AF2545	hypothetical prote
42	72	7.9	255	2 F81033	conserved hypothet
43	72	7.9	255	2 E81197	hypothetical prote
44	72	7.9	2 A70081	conserved hypothet	
45	72	7.9	351	2 S74651	hypothetical prote

ALIGNMENTS

RESULT 1	A38580	interleukin-10 precursor - human
		alternative name: cytokine synthesis inhibitory factor (CSIF); IL-10
		C-Species: Homo sapiens (man)
		C-Date: 14-Feb-1992 #text_change 09-Jul-2004
		C-Accession: A38580; G01539; I549110; I37890
		R-Vieira, P.; de Waal-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Fiorentini, Proc. Natl. Acad. Sci. U.S.A., 88, 1172-1176, 1991
		A-Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA c
		A-Reference number: A38693; MUID:9142134; PMID:1847510
		A-Accession: A38580;
		A-Molecule type: mRNA
		A-Residues: 1-178 <VIE>
		A-Cross-references: UNIPARC:UPI000034E50; GB:W57627; NID:9186270; PMID:9186270
		R-Windsor, W.T.; SYTO, R.; Tsarhopoulos, A.; Zhang, R.; Durkin, S.; Palivis, J.; Baldwin, S.; Paliogianni, Biochemistry, 32, 8807-8815, 1993
		A-Status: preliminary; disulfide bonds and secondary structure analysis of human and murine interleukin-10 precursor
		A-Title: Disulfide bond assignments and secondary structure analysis of human and murine interleukin-10 precursor
		A-Reference number: A48693; MUID:9142134; PMID:1847510
		A-Contents: annotation; disulfide bonds in recombinant protein
		A-Samianwala, B.
		submitted to the EMBL Data Library, October 1994
		A-Reference number: G07695
		A-Accession: G01539
		A-Status: translated from GB/EMBL/DDBJ
		A-Molecule type: DNA
		A-Residues: 1-178 <VIE>
		A-Cross-references: UNIPARC:UPI000034E50; EMBL:U16720; NID:9141812; PMID:AAA8104.1;
		R-Kube, D.; Platzer, C.; von Knethen, A.; Straub, H.; Hafner, M.; Tesch, H.
		A-Description: Isolation of the human interleukin-10 promoter. Characterization of the A-Reference number: S49110
		A-Accession: S49110
		A-Status: preliminary
		A-Molecule type: DNA
		A-Residues: 1-6 'PVAVSS' <KUB>
		A-Cross-references: UNIPARC:UPI0000178477; EMBL:X78437; NID:91167482
		R-Platzer, C.; Volk, H.D.; Platzer, M.
		A-Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walk
		A-Reference number: 137890; MUID:95143580; PMID:7841462
		A-Accession: I37890
		A-Status: preliminary; translated from GB/EMBL/DDBJ
		A-Molecule type: DNA
		A-Residues: 1-6 <PLA>
		A-Cross-references: UNIPARC:UPI000011E989; EMBL:X73536; NID:9452395; PMID:CAA51942.1;
		C-Genetics:
		A-Gene: GDB:IL10; IL-10
		A-Cross-references: GDB:128636; OMIM:124092
		A-Map position: 1q31-1q32
		A-Map position: 1q31-1q32
		A-Introns: 55/3; 75/3; 12/3; 14/3
		C-Superfamily: interleukin-10

N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
 C;Accession: A34853; I56136
 R;Moore, K.W.; Vieira, P.; Florentino, D.F.; Trounstein, M.L.; Khan, T.A.; Mosmann, T.R.;
 Science, 248, 1230-1234, 1990
 A;Title: Homology of cytokine synthesis inhibitory factor (IL-10) to the Epstein-Barr virus
 A;Reference number: A34853; MUID:90273182; PMID:2161559
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-178 <MO>
 A;Cross-references: UNIPROT:P18833; UNIPARC:UPI00002149E; GB:M37897; NID:918288; PIDN:
 R;Kim, J.M.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.;
 J. Immunol. 148, 3618-3623, 1992
 A;Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse and
 A;Reference number: I56136; MUID:92268508; PMID:1350294
 A;Accession: I56136
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-178 <RES>
 A;Cross-references: UNIPARC:UPI00002149E; GB:MB4340; NID:9198291; PIDN:AAA39275.1; PID:
 A;Genes: IL10
 A;Introns: 55/3; 75/3; 126/3; 149/3
 C;Superfamily: interleukin-10
 C;Keywords: cytokine; lymphokine; T-cell
 Query Match 15.8%; Score 144; DB 2; Length 178;
 Best Local Similarity 31.1%; Pred. No. 1.3e-06; Mismatches 53; Conservative 19; Indels 6; Gaps 4;
 Matches 42; Conservative 19; Mismatches 68; Indels 6; Gaps 4;
 Qy 39 LOEIRNGFSDIRGSVQAKQNDITRILRRTESLODTPKPNRCCLLRHLRLYDRVFKNY 98
 Db 41 LLELRTAFSQVKTFQTKO-OLD-NILITDSLMQDPKGIGQALSEMIQFLVEMRQA 98
 Qy 99 QTPHYTURKISSLANSFETIKKDLCHAHMTCHGEGEAMKKYQIISHSPEKLEPOANV 158
 Db 99 EKIGPEIHKHLNSLGEKLTMLRMURRCHRFPLC---ENKSKAVEQVKSDFNKLQD-GV 154
 Qy 159 VKAGLBELDITLQWME 173
 Db 155 YKANNEFDIFINCIE 169
 Qy 164 FINCIE 169

RESULT 6
 JN0475
 N;Alternate name: cytokine synthesis inhibitory factor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: JN0475; JG1357; S36021
 R;Feng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B.
 Biochem. Biophys. Res. Commun. 192, 452-458, 1992
 A;Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and
 A;Reference number: JN0475
 A;Accession: JN0475
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-178 <FEN>
 A;Cross-references: UNIPROT:P29556; UNIPARC:UPI0000167959
 R;Goodman, R.E.; Oblak, J.; Bell, R.G.;
 Biochem. Biophys. Res. Commun. 189, 1-7, 1992
 A;Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from the
 A;Reference number: JG1357; MUID:93080542; PMID:1280414
 A;Accession: JG1357
 A;Molecule type: mRNA
 A;Residues: 1, p, 3-64, 'L', 66-178 <GOO>
 A;Cross-references: UNIPARC:UPI000012D477; GB:L02926; NID:9204903; PIDN:AAA41425.1; PID:
 R;Feng, L.; submitted to the EMBL Data Library, July 1991
 A;Accession: S36021

RESULT 7
 JC5538
 Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
 C;Accession: JC5538
 R;Song, H.J.; Rosei, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.
 Biochem. Biophys. Res. Commun. 235, 10-14, 1997
 A;Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutaminase
 A;Reference number: JC5538; MUID:97339427; PMID:916026
 A;Accession: JC5538
 A;Molecule type: DNA
 A;Residues: 1-567 <SON>
 A;Cross-references: UNIPROT:Q92696; UNIPARC:UPI000013188E
 C;Comment: This protein is involved in cutaneous disease. The gene of this enzyme is p
 C;Keywords: transferase
 A;Gene: Rabgta
 A;Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 41
 C;Genetics:
 A;Cross-references: UNIPROT:Q92696; UNIPARC:UPI000013188E
 C;Comment: This protein is involved in cutaneous disease. The gene of this enzyme is p
 C;Keywords: transferase
 Query Match 10.4%; Score 94.5; DB 2; Length 567;
 Best Local Similarity 25.8%; Pred. No. 0.35; Mismatches 49; Conservative 26; Gaps 9;
 Matches 49; Conservative 26; Mismatches 82; Indels 33; Gaps 9;
 Qy 1 MKASSAFLSLSAAYFLWTPSTGKTNLGSCVATNLOE--IRGFSID--IRGSVA 55
 Db 304 LPAAASLNDOLPQHTFPRVIVTAWGDVQK----ECLVLRQEGWCRDSTIDEOLFR CELSV 358
 Qy 56 KQDNTIDIRRLRRTESLODTPKPNRCCLLRHLRLYDRVFKNYQT---PDH 103
 Db 359 EKSTVLOSBLESCKELOBLPENKWLITILMRLDPLPYEKETLQYFOTLKVADPMR 418
 Qy 104 YT---LKKISSLANSFETIK---KDLCHAHMTCHGEGEAMKKYQI-LSH--FEKL 152
 Db 419 ATVLDLRSKELLENSVVKMVEAERVVHLANKDLTVLCHLQFQIYVHLDISHNRTL 478
 Qy 153 EPOQAVVAK 162
 Db 479 PPALALRCL 488

A45977 Rab geranylgeranyl transferase component B alpha subunit - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 16-Feb-1994 #sequence_change 09-Jul-2004

C;Accession: A45977

R;Armstrong, S.A.; Sebra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.

J. Biol. Chem. 268, 12221-12229, 1993

A;Title: cDNA cloning and expression of the alpha and beta subunits of rat Rab geranylger

A;Reference number: A45977; MUID:9328021; PMID:8505342

A;Accession: A45977

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-1567 <ARM>

A;Cross-references: UNIPROT:Q08602; UNIPARC:UPI000013188F; GB: S62096; NID:9385474; PIDN:

A;Note: sequence extracted from NCBI backbone (NCBIN:133369, NCBIPI:133370)

Query Match 10.4%; Score 94.5; DB 2; Length 567;

Best Local Similarity 24.2%; Pred. No. 0.35; Mismatches 80; Indels 33; Gaps 8;

Matches 46; Conservative 31; Mismatches 80; Indels 33; Gaps 8;

Oy 1 MKQASSLAFSLSAAFLYLWPTSTGLTKTLNGLGCVIATNLQE--IRNGFSD--IRGSVQA 55

Db 304 LPANSINPOLQPTFRVWIGPSQK---ECVLUKORPCEWCDSATDEQFLRCESV 358

Oy 56 KDGNDIIRTRRERESLQDTKPAWCCLRLHLL-YLDRVKPKYQTPDHYT----- 105

Db 359 EKSTVQLSBLESCKELOELEPKWCLLITILMRAUDPLVYKETLQYFSTLKVADPMR 418

Oy 106 ---IRKISSLANSFLIK---KOLRICHAMTCGEGEAMKVKSYQLISH-FEKL 152

Db 419 AAYVLDLLESKFLLENSVLUKMEVADVRVLHLAKDLTVLCHLSEQLVYHDLISHNRLR 478

Oy 153 EPOAVVVKAL 162

Db 479 PPALAAUCL 488

RESULT 9

64594 probable beta-adaptin YKSS - yeast (*Saccharomyces cerevisiae*)C;Species: *Saccharomyces cerevisiae*

C;Date: 17-May-1996 #sequence_change 17-May-1996 #text_change 09-Jul-2004

C;Accession: S64594; S63450

R;Panzica, L.; Agostoni, Carbone, M.L.; Melchiorotto, P.; Plevani, P.; Martegani, E.; Var

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64591

A;Accession: S64594

A;Molecule type: DNA

A;Residues: 1-109 <PAN>

A;Cross-references: UNIPROT:P46682; UNIPARC:UPI0000530A8; EMBL:Z73046; NID:91323474; PI

A;Experimental Source: strain S288C

R;Robinson, L.C.; Engle, H.M.; Panek, H.R.

Submitted to the EMBL Data Library, September 1995

A;Description: Suppressors of loss of yeast casein kinase 1 function define the four sub

A;Reference number: S63439

A;Accession: S63430

A;Molecule type: DNA

A;Residues: 1-26, 'PLSWINRPP', 36-723, 'T', 725-795, 801-809 <ROB>

A;Cross-references: UNIPARC:UPI0000168A41; EMBL:U35411; NID:g1017728; PID:g1017729

A;Map position: 7R

Query Match 10.3%; Score 93.5; DB 2; Length 809;

Best Local Similarity 24.1%; Pred. No. 0.66; Mismatches 48; Conservative 39; Indels 39; Gaps 10;

Oy 2 KASSLAFSLSAAYFLWPTSTGKTLNGLGCVIATNLQEIRNGFSDIRGVSQAKDSD 61

Db 21 EAAAVATSKLGESSYYTYY--SONINPQQLWTLINNSRNSRVRDAMKRISIMASDDDSID 78

Qy 62 IRI---LRRTESTLQDTKPAWCCLRLHLLYLDVFKNQTPDHYTURKISSLANSPL 117

Db 79 VOLYFADVKNITNDIK-----VRLHLYLRLPAEN--DPNLTLLSINSLQLSLS 128

Oy 118 TTKDRLCHAMTCGEGEAMKVKSYQLSHEK--LEPQ-----AVVK-AIGE 164

Db 129 DSNSEL-CFA--LSALSDMKSSLAPILHVTVKLVTDPSAMVRGEVALATIKLYRAGK 185

Oy 165 -----LDLILQWMETE 176

Db 186 NYHEEDLIDILKEIMADTD 204

RESULT 10

F3128

probable transcription regulator PA4135 [imported] - *Pseudomonas aeruginosa* (strain PA01)C;Species: *Pseudomonas aeruginosa*

C;Accession: F83128

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brinkman, F.S.; Adams, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A;Reference number: A82950; MUID:2043737; PMID:10984043

A;Accession: F83128

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140 <STO>

A;Cross-references: UNIPROT:Q9JWP6; UNIPARC:UPI00000C5C2C; GB:AE004830; GB:AE00491; NI

A;Experimental source: strain PA01

C;Genetic:

A;Gene: PA4135

RESULT 11

T33346

hypothetical protein C16A11.5 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Accession: T33346

C;Date: 29-Oct-1999 #sequence_change 29-Oct-1999 #text_change 09-Jul-2004

R;Johnson, D.; Biewald, T.

submitted to the EMBL Data Library, July 1998

A;Description: The sequence of C. elegans cosmid C16A11.

A;Reference number: 221328

A;Accession: T33346

A;Status: preliminary; translated from GB/EMBL/DDAJ

A;Molecule type: DNA

A;Residues: 1-646 <JDR>

A;Cross-references: UNIPROT:O75579; UNIPARC:UPI0000076553; EMBL:AF077536; PIDN: AAC26261

A;Experimental Source: strain Bristol N2; clone C16A11

C;Genetics:

A;Gene: CEGP-C16A11.5

A;Map position: 2

A;Introns: 35/3; 72/1; 94/3; 129/3; 184/3; 205/1; 279/3; 387/3; 505/2; 540/2; 570/3

Query Match 9.0%; Score 81.5; DB 2; Length 646;

Best Local Similarity 26.1%; Pred. No. 7.5; Mismatches 36; Conservative 22; Indels 49; Gaps 31; Gaps 8;

Oy 21 EAAAVATSKLGESSYYTYY--SONINPQQLWTLINNSRNSRVRDAMKRISIMASDDDSID 78

Qy 29 NLGSCVINTLQEQIRNGGSDPIRSVQAKDGNIDIRILR-----RTELSQDTKPARC 80
 Db 176 NDGACFVDRSLSQ-RNSNCDHPLVQDLSMSKSFIEQHPIRAKHKVAPIRDLSKPCSYC 234
 Qy 81 CL-LRHLLRLYLD----RUVFKVQQTPOD-HYTLLRKISSLANSFLTIKKDRULCHALMTC 132
 Db 235 ILAVDALFELFNTIWIQSERVFERHKVPKLIEYVL-KIPT----LLFKSELRRPHFVTKA 288
 Qy 133 HCGBEAMKRYKSYOILSHFE 150
 Db 289 H-----LHLILASFE 298

RESULT 12

Q46367 protein kinase CDC7 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-Oct-2004
 C;Accession: S46367; T39888
 R;Frankhauser, C.; Simanis, V.
 EMBL J. 13 3011-3019 1994
 A;Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation in
 A;Reference number: S46367; MUID:94313982; PMID:8039497
 A;Accession: S46367
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-1062 <PAN>
 A;Cross-references: UNIPARC:PA1892; UNIPARC:UPI0000127259; EMBL:X78799; NID:9521098; PID:AD3160
 A;Experimental source: wild-type 972 h minus
 A;Note: mRNA Sequencing was also done to confirm the intron borders
 R;Saunders, D.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, February 1999
 A;Reference number: 221860
 A;Accession: T39888
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Gene: CDC7; SPDB:SPBC21.06C
 A;Map position: II: 2
 A;Introns: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3
 C;Function:
 A;Cross-references:
 C;Experimental source: strain 972h; cosmid c21
 C;Genetics:
 A;Gene: CDC7; SPDB:SPBC21.06C
 A;Map position: II: 2
 A;Introns: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3
 C;Function:
 A;Description: essential for septum formation and cell division
 C;Keywords: ATP; cell division; phosphotransferase; protein kinase
 F7-239/Domain: protein kinase homology <KIN>
 F7-23/Region: protein kinase ATP-binding motif

Query Match 8.9%; Score 81; DB 2; Length 1062;
 Best Local Similarity 30.4%; Pred. No. 15; Indels 32; Conservative 20; Mismatches 44; Gaps 4;
 Matches 32; Gaps 4; Indels 10; Gaps 4;

Qy 23 TGLKTLNIGSCVINTLQEQIRNGGSDPIRSVQAKDGNIDIRILRRLRTESTQDTPKPARC 81
 Db 466 TGLGTLVNLKCYGSWNNEBESDIDFSDTENLNDIE----NNIALDKRTHLAS 520
 Qy 82 LIRHLRLYLDLDRFKVQQTPOD-HYTLLRKISSLANSFLTIKKDRULCH 127
 Db 521 LASSLSSLSDR--KNGSKD-TTVQCLASLISEDLSKRELIOAH 562

RESULT 13

T19925 hypothetical protein C44C10.4 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Accession: T19925
 C;Date: 15-Oct-1995 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R;Cottage, A.
 submitted to the EMBL Data Library, February 1996
 A;Reference number: 219197
 A;Accession: T19925
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match 8.8%; Score 80; DB 2; Length 542;
 Best Local Similarity 23.2%; Pred. No. 8; Gaps 5; Indels 28; Gaps 4;
 Matches 29; Conservative 25; Mismatches 43; Indels 28; Gaps 4;

Qy 39 LQFIRNGGSDPIRSVQAKDGNIDIRILRTESTQDTPKPARCCLLRHLRLYLDVPKNY 98
 Db 212 IQTKEKEVAAEQLKVNAGAKQPLRISYERIPKQTPSPN----FKN 256
 Qy 99 -----OPRDHY---TURKISSLANSFLTIKKDRULCHGCEAMKQYSQI 145
 Db 257 ATVURPKTHNHYDNLITVDKLNSYLNKSVTERRELLQPAVNHPNMNRFSEBGPNTIARE 316
 Qy 146 LSHFE 150
 Db 317 IDTPE 321

RESULT 14

AD3160 hypothetical protein glnp/glnq [imported] - Agrobacterium tumefaciens (strain C58, Duster, E.W.)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AD3160
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.; Science, 294, 2317-2323, 2001
 A;Author: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A;Cross-references: UNIPARC:UPI0000127259; EMBL:AL035537; PIDN:CAB36886.1; GSPDB:GN00067
 A;Experimental source: strain C58 (Dupont)
 A;Genetics:
 A;Gene: glnp/glnq
 A;Map position: II: 2
 A;Introns: 1-502 <KUR>
 C;Function:
 A;Cross-references:
 A;Experimental source: strain C58 (Dupont)
 A;Genetics:
 A;Gene: glnp/glnq
 A;Genome: plasmid

Query Match 8.8%; Score 76.5; DB 2; Length 502;
 Best Local Similarity 24.6%; Pred. No. 17; Indels 42; Conservative 23; Mismatches 37; Gaps 10; Matches 42; Gaps 10; Indels 69; Gaps 10;

Qy 10 LLSAAFPILWT-PSTGL----KTLNLGS---CVIATNQEQIRNGGSDPIRSVQAKDGNIDIRILRRLRTESTQDTPKPARC 55
 Db 206 LLAGFVLLIVTPVPLRHYNAIDNRLRIGKQPSVITSGLEV--SELDGARASCVAF 261
 Qy 56 KDGNDTDIRLRLRTESTQD-----TKPKPARC----LIRHL-----86
 Db 262 KGDSLDRVRLGMAYGGLDVLKGVDLSVKPGSVCILGPGSGSKSTLRLGLNLVPEPKSGD 321
 Qy 87 -----LALYLDRFKVQQTPOD-HYTLLRKISSLANSFLTIKK 121
 Db 322 ILTDGESLTLAKPETLRRVGMWFOHNLFPDH----TALENVWLSLKK 366

RESULT 15

B90153 2-isopropylmalate synthase, probable (leuA-1) [imported] - *Sulfolobus solfataricus*
 C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: B90153

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, E.; R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to Genbank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A9139
A;Accession: B90153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-553 <KUR>
A;Cross-references: UNIPROT:Q98021; UNIPARC:UPI000006418D; GB:AE006641; NID:gi13813259; E

C;Genetics:
A;Gene: leuA-1
C;Superfamily: 2-isopropylmalate synthase leuA
Query Match 8.4%; Score 76.5; DB 2; Length 553;
Best Local Similarity 19.6%; Pred. No. 19;
Matches 39; Conservative 34; Mismatches 61; Indels 65; Gaps 8;
Matches 39; Conservative 34; Mismatches 61; Indels 65; Gaps 8;
Qy 24 GLKTYLNLGSCVIAVNLOSTRNGSDIRGSVQA--KGSNID-----IRIRR 67
Db 232 GIAHAKNDIGCAVANSLMAIKAGARHVGQTINGIGERTGSNADLIQIIPFLIKNGLNALNG 291
Qy 68 TESIQLQPTIPANRCC-----LIRHHLRILYIDQDRVKYQVQTPDH----- 103
Db 292 QESLRKLRVSRIVTEVILGLPPNPYQPYVGDNAFAHKAGVHDAVMKVPRAYEVHDPSSLV 351
Qy 104 -----YTRKISSLAN--SFL-----TIKDQURLCHAHMTCHGEBAKQYSQILSHFE 150
Db 352 GNDRKFKVISELSGTPANLYSYLOGLGIAYDKDRRL-----KRAKNIKKELERGY 401
Qy 151 KLB--POAVVKALGELDI 167
Db 402 SFDVGPASAILITKEINI 420

Search completed: December 24, 2005, 10:28:05
Job time : 18 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
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<http://www.pir.uniprot.org/database/archive.shtml>

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John C. [unclear]

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GenCore version 5.1.6

OM protein - protein search, using SW model
Run on: December 24, 2005, 10:26:03 ; Search time 228 Seconds
Sequence: 1 MKASSLAFSLISAAYLLNT.....AVVKAGELDILLOWMEEET 176

Title: US-10-789-251-2
perfect score: 910
Sequence: 1 MKASSLAFSLISAAYLLNT.....AVVKAGELDILLOWMEEET 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : UniProt 05_80:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description
1	906	99.6	176	1	IL20_HUMAN	Q9YV11 homo sapien
2	672	73.8	176	1	IL20_MOUSE	Q9JXK9 mus musculus
3	37.5	37.1	177	1	IL19_HUMAN	Q9HWD0 homo sapien
4	337.5	37.1	215	2	Q5V0T3_HUMAN	Q9VUT3 homo sapien
5	306	33.6	168	2	Q4LDR4_BZIPARE	Q1dr4 brachydano
6	281.5	30.9	176	1	IL19_HUMAN	Q8CJ50 mus musculus
7	266.5	29.3	175	2	Q7SX60_TETNG	Q8X60 tetradein
8	222.2	24.4	220	2	Q92KJ3_MOUSE	Q92KJ3 mus musculus
9	220	24.4	181	2	Q92S4_MOUSE	Q92S4 mus musculus
10	217	23.8	206	1	IL24_HUMAN	Q3J007 homo sapien
11	217	23.8	207	1	Q53Z77_HUMAN	Q3X2Z7 homo sapien
12	191	21.0	183	1	MOB5_RAT	Q9j124 rattus norvegicus
13	187	20.5	183	2	Q9WTF8_RAT	Q9wfp8 rattus norvegicus
14	175.5	19.3	175	2	Q6A2H5_CHICK	Q8a2h5 gallus gallus
15	175	19.3	175	2	Q6A2H4_CHICK	Q8a2h4 gallus gallus
16	161.5	17.7	178	1	IL10_MACNE	Q8a197 macaca nemestrina
17	161	17.7	177	1	Q8UJ16_MACMA	Q8uji6 cercopithecus aethiops
18	157.5	17.3	178	1	IL10_MACCPA	Q8p938 macaca fasciata
19	157.5	17.3	178	1	IL10_MACM	Q8p946 macaca mulatta
20	157.5	17.3	178	1	IL10_PAPRA	Q8q0v6 papio hamadryas
21	157.5	17.3	180	2	Q7T3J1_CYPCHA	Q8t3j1 cyprinus carpio
22	156.5	17.2	160	2	Q7IUZ1_HUMAN	Q8iuz1 homo sapien
23	156.5	17.2	178	1	IL10_FELCA	Q85029 felis silvestris
24	156.5	17.2	178	1	IL10_HUMAN	Q82301 homo sapien
25	156.5	17.2	178	2	Q6F5W4_HUMAN	Q8f5w4 homo sapien
26	155	17.0	170	1	IL10_EBV	Q8j180 Epstein-Barr virus
27	155	17.0	170	2	Q77H29_CAMA	Q877h2 cambarus
28	155	17.0	175	1	IL10_PIG	Q82905 sus scrofa
29	154.5	17.0	178	1	IL10_CERTO	Q846651 cercopithecus aethiops
30	153	16.8	178	1	IL10_MERIN	Q87965 meriones unicolor
31	151.5	16.6	179	1	IL10_CERBEL	Q81746 cervus elaphus

ALIGNMENTS

32	151	16.6	178	1	IL10_RABBIT	Q8t8j4 oryctolagus cuniculus
33	147.5	16.2	178	2	Q9TWD3_RABBIT	Q8twd3 oryctolagus cuniculus
34	147.5	16.2	179	1	IL10_EHWT2T	Q86577 equine herpes virus
35	147.5	16.2	179	1	IL10_EHWT	Q86893 mus musculus
36	147	16.2	178	1	IL10_MOUSE	Q86599 homo sapiens
37	145.5	16.0	178	2	Q923T1_SIGM1	Q823t1 sigma-1
38	144.5	15.9	160	2	Q923T1_SIGM1	Q823t1 sigma-1
39	144.5	15.9	174	1	IL10_TRIVU	Q87798 trichosurus vulpecula
40	144.5	15.9	178	1	IL10_HORSE	Q82837 equus caballus
41	143.5	15.8	178	2	Q6VV71_BOBBU	Q86vv71 bubalus bubalis
42	143	15.7	171	2	Q90511_CHV12	Q8q511 cercopithecus aethiops
43	142.5	15.7	178	2	Q8WMK9_SAISC	Q8wmk9 saimiri sciureus
44	142.5	15.7	178	2	Q8WMK9_SAISC	Q8wmk9 saimiri sciureus
45	142	15.6	181	1	IL10_CANFA	Q848411 canis familiaris

DR SMART: SM00188; IL10; 1.
 DR PROSITE: PS00520; INTERLEUKIN_10; 1.
 KW Cytokine; Signal.

FT SIGNAL 1 24 Potential.
 FT CHAIN 25 176 Interleukin-20.
 FT DISULFID 33 126 Potential.
 FT DISULFID 80 132 Potential.
 FT DISULFID 81 134 Potential.

SO SEQUENCE 176 AA; 20098 MW; 08577AF665657471 CRC64;

Query Match 73.8%; Score 672; DB 1; Length 176;
 Best Local Similarity 75.3%; Pred. No. 1 5e-57;
 Matches 131; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MKASSLAFSLSAFAFLWLTPTSTGLKTNLNGSCVIAITNLQIRNGSDIRGSVQAKGNI 60
 Db 1 MKGFGLAFLGFLFSAVGLFLWTLPLGLKTNLNGSCVITANLQIAQKEFSBIRDVOAEDTN 60

Qy 61 DTRILRRTESLQDTKPNRCCRLRHLRLYDVRPKYQTPDHYTURKISSJANSFTIK 120
 Db 61 DTRILRTESLQDTKOSLRCRFLRHFYFLDVKYQTPDHYTURKISSJANSFTIK 120

Qy 121 KDLRLCHAHMTCHGEEAKKYSQISLSHFEKELPQAAVVKALGELDILQWME 174
 Db 121 KOLSVCHSHMACHGEEAKMKNQILSHFIELQAAVKALGELGILRME 174

RESULT 3

IL19_HUMAN STANDARD; PRT: 177 AA.

AC Q960R4; Q9NUK0; [6]
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Interleukin-19 precursor (IL-19) (Melanoma differentiation associated protein-like protein) (NG_1).
 DE Name=IL19; Synonyms=2MDA1;
 OS Homo sapiens (Human).
 OC Bukaryota; Metacarta; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OC HOMO. OX _ TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 MEDLINE=21040165; PubMed=1196675; DOI=10.1038/sj.j gene.6363714;
 RA Gallagher G., Dickensheets H., Bokdale J., Izotova L.S.,
 RA Mirochnitschenko O.V., Peat J.D., Vasquez N., Donnelly R.P.,
 RA Kotenko S.V.;
 RT "Cloning, expression and initial characterization of interleukin-19 (IL-19), a novel homolog of human interleukin-10 (IL-10).";
 RL Genes Immun. 1:442-450(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 MEDLINE=22257669; PubMed=12370360;
 RA Liao Y.-C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.-S.,
 RT "IL-19 induces production of IL-6 and TNF-alpha and results in cell apoprosis through TNF-alpha.;"
 RL J. Immunol. 169:4288-4297(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Conklin D., Petersen J., Lofton-Day C., Whitmore T., Muerer M.,
 RA "Homo sapiens homolog of melanoma differentiation gene.;"
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Kotenko S.V., Peatka S.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT PHE-175.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-

FT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PROTEIN SEQUENCE OF 25-39.
 RA PubMed=15340161; DOI=10.1101/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites." RT
 RL Protein Sci. 13:2819-2824(2004).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 19-177, AND DISULFIDE BONDS.
 RX PubMed=12403790; DOI=10.1074/jbc.M208602200;
 RA Chang C., Magracheva B., Kozlov S., Fong S., Tobin G., Kotenko S., Wlodawer A., Zdanov A.;
 "Crystal structure of interleukin-19 defines a new subfamily of helical cytokines.;"
 RL J. Biol. Chem. 278:3308-3313 (2003).
 CC -i- FUNCTION: May play some important roles in inflammatory responses.
 CC -i- UP-regulates IL-6 and TNF-alpha and induces apoptosis (By similarity).
 CC -i- SUBCELLULAR LOCATION: Secreted.
 CC -i- SIMILARITY: Belongs to the IL-10 family.

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CC -i- DR AF276915; AAGI6755.1; -; Genomic_DNA.
 CC -i- DR EMBL; AF453946; AANQ0906.1; -; mRNA.
 CC -i- DR EMBL; AF404367; AAK91776.1; -; mRNA.
 CC -i- DR EMBL; AP390905; AAKG4498.1; -; Genomic_DNA.
 CC -i- DR EMBL; AL059613; CABY2342.1; -; Genomic_DNA.
 CC -i- DR PDB; 1NLF; X-ray; A=19-177.
 CC -i- DR Ensemble; ENSG00000142224; Homo sapiens.
 CC -i- DR HGNC; 5990; IL19.
 CC -i- DR MIM; 605687; -.
 CC -i- DR GO; GO:00052576; C:extracellular region; NAS.
 CC -i- DR GO; GO:0005125; P:cytokine activity; TAS.
 CC -i- DR GO; GO:0006955; P:immune response; NAS.
 CC -i- DR GO; GO:0007165; P:signal transduction; NAS.
 CC -i- DR InterPro; IPR002351; Cytokine 4_hk.
 CC -i- DR InterPro; IPR000098; Interleukin_10.
 CC -i- DR Pfam; PF00726; IL10; 1.
 CC -i- DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 CC -i- DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 KW 3D-structure; Apoptosis; Cytokine; Direct protein sequencing;
 KW Glycoprotein; Apoptosis; Cytokine; Signal.

FT SIGNAL 1 24 Interleukin-19.
 FT CHAIN 25 177 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHY 56 56 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHY 135 135 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 28 121
 FT DISULFID 75 127
 FT DISULFID 76 129
 FT DISULFID 175 175 S -> F
 FT VARIANT 177 AA; 20392 MW; /FTID=VAR013077; CRC64;
 SO SEQUENCE 177 AA; 20392 MW; /FTID=VAR013077; CRC64;

Query Match 37.1%; Score 337.5; DB 1; Length 177;
 Best Local Similarity 39.7%; Pred. No. 9.4e-25;
 Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;

Qy 1 MKASSLAFSLSAFAFLWLTPTSTGLKTNLNGSCVIAITNLQIRNGSDIRGSVQAKGNI 60
 Db 1 MLUQCLSLWLGTTILCLCSVNQH----RCLISTDMHIEESQEIRKAIQKDTPE 55

RT "Evolution of IL-10 family genes in teleosts.";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB219579; BAE0181..1; -; mRNA.
 SQ SEQUENCE 168 AA; 19110 MW; 807D18AD736C709B CRC64;

Query Match 33.64; Score 306; DB 2; Length 168;
 Best Local Similarity 42.44; Pred. No. 1..1e-21; Mismatches 58; Indels 6; Gaps 3;

Matches 67; Conservative 27;

RESULT 4
 OSVUT3 HUMAN HUMAN PRELIMINARY; PRT; 215 AA.
 ID OSVUT3;
 AC 05VUT3;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Interleukin 19.
 Name=IL19; ORFNames=RRI1-262N9.2-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Buarchoontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 DR NCBI_TaxID=9606;
 RN 1119_MOUSE
 RP NUCLEOTIDE SEQUENCE.
 RA Kay M.;
 RL Submitted (MAY-2005) to the BMBL/GenBank/DBJ databases.
 CC -; SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; AL513115; CAH71814..1; -; Genomic_DNA.
 DR SRR; OSVUT3; 60..215;
 DR Ensembl; ENSG00000142224; Homo sapiens.
 DR GO; GO:0005115; C:extracellular space; IEA.
 DR GO; GO:005123; P:immune response; IEA.
 DR GO; GO:006355; P:immune response; IEA.
 DR InterPro; IPR00098; Interleukin_10.
 DR Pfam; PF0726; IL10..1.
 DR PROSITE; PS00520; INTERLEUKIN_10; UNKNOWN_1.
 DR KW Cytokine.
 SQ SEQUENCE 215 AA; 24567 MW; D79D610P11DA74E4 CRC64;

Query Match 37.1%; Score 337.5; DB 2; Length 215;
 Best Local Similarity 39.7%; Pred. No. 1..2e-24; Mismatches 69; Conservatism 36; Indels 5; Gaps 1;

CC 1 MKASSLALSILSAFAVLUWTPSTGLKTLNGSCVIAATLQLEIRNGFSDIRGSVQAKGNI 60
 DR 39 MKIQCQVSLWLGTLILCSVDNHGILR----RECLISTDNHHTESFQPIKRAIQAKOTFP 93

Query Match 61 DIRILRRTESLQDTKPAKRCCLRLRLYDRVFKNYQTDPHILRKTSILANSFLTIK 120
 DR 94 NVTILSTLTLQTIKPLDVQCVVTKLILAFYDVRFKQDQPNPKLRKTSIANSFLYQ 153

Query Match 121 KDIRLCHARTCHGCGEAMKKYQSLISLPEKLSRPAQAVVKAQGBLDLQNMRE 174
 DR 154 KTLRQCOBORGCHCROATNATRVIHDNYDQLEVHAAIKSLGELDVFLAWINK 207

RESULT 5
 QALDR4 BRAKE PRELIMINARY; PRT; 168 AA.
 ID QALDR4;
 AC 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Interleukin 10 family protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 DR NCBI_TaxID=7955;
 RN [1] NUCLEOTIDE SEQUENCE.
 RA Ram S., Daisuke I., Sakai M.;

RESULT 6
 III19_MOUSE STANDARD; PRT; 176 AA.
 ID III19_MOUSE
 RP NUCLEOTIDE SEQUENCE, AND FUNCTION.
 RC STRAIN-SWISS Webster / NIH;
 RX MEDLINE=22257669; PubMed=12370360;
 RA liao Y-C., Liang W-G., Chen F-W., Hsu J-H., Yang J-J., Chang M.-S.;
 RT "IL-19 induces production of IL-6 and TNF-alpha and results in cell
 apoptosis through TNF-alpha.";
 RL J. Immunol. 169:4288-4297(2002).
 CC -; SUBCELLULAR LOCATION: Secreted.
 CC -; SIMILARITY: Belongs to the IL-10 family.
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 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; AP453345; RAN40905.1; -; mRNA.
 DR HSSP; Q9UHD0; 1NIP.
 DR SDR; Q8CJ70; 23..170.
 DR Ensembl; ENMG00000016524; Mus musculus.
 DR GO; GO:0006317; P:induction of apoptosis; IDA.
 DR GO; GO:0042226; P:interleukin-6 biosynthesis; IDA.
 DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
 DR InterPro; IPR01251; Cytokine_4_helix.
 DR InterPro; IPR00098; Interleukin_10.
 DR ProDom; PDD03687; Interleukin_10.
 DR SMART; SM00188; IL10..1.
 DR PROSITE; PS00520; INTERLEUKIN_10; FALSE NEG.
 DR KW Apoptosis; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 176 Interleukin_19.
 FT CARBOHYD 56 56 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 134 134 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 28 120 By similarity.
 FT DISULFID 74 126 By similarity.
 FT DISULFID 75 128 By similarity.
 SQ SEQUENCE 176 AA; 20288 MW; 7386C1HC54077FDC CRC64;

Query Match 30.9%; Score 281.5; DB 1; Length 176;
 Best Local Similarity 38.6%; Pred. No. 2.9e-19; DB 1;
 Matches 56; Conservative 35; Mismatches 53; Indels 1; Gaps 1;
 Ov 29 NLGSCVIATNLQBIKRSFDIRGSVQAKGNDIDIRLRTESLOPDKPANRCLLHR 88

Db 24 SLRRLCLISDVMLRLEKSFHFKRANKTQTKPFKNVIL-SLENLRSIKPQDVCCMNNLT 82

Ov 89 LYLRVFKYQTPHYTIKISSLANSPTIKQDRLCHAHMICHGEBAMKYSQILH 148

Db 83 PYRDRVFQHQHQSLEVLKRISSTNLSPVQKSLERCOVHQRCNCSDATNATRHH 142

Ov 149 PEKLEPOQAAVVKALGELDILLOMME 173

Db 143 YNQLEVSSALKSLSGELNLLAWID 167

RESULT 7

Q7SX60_TETNG PRELIMINARY; PRT; 175 AA.

ID Q7SX60_TETNG PRELIMINARY; PRT; 175 AA.

AC 01-OCT-2003 (Tremblel. 25, Created)
 DT 01-OCT-2003 (Tremblel. 25, Last sequence update)
 DT 01-FEB-2005 (Tremblel. 29, Last annotation update)
 DE Interleukin-20.
 GN Name=IL20;
 OS Tetradon nigroviridis (Green puffer)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Actinopterygii; Acanthopterygii; Teleostei; Neoteleostei;
 OC Tetradontoidea; Tetraodontidae; Tetradon.
 OX NCBI_TaxID=99883;
 RN [1];
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/C;
 RX MEDLINE-21240641; Pubmed=11342597;
 RA Schaefer G., Venkataraman C., Schindler U.;
 RT "FISP (IL-4-induced secreted protein), a novel cytokine-like molecule
 RT secreted by Th2 cells";
 RL J. Immunol. 166:859-863 (2001).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL, AF33251; AAK5270.1; mRNA.
 DR Ensembl; ENSEMBL0000026420; Mus musculus.
 DR MG1; MG1:2135548; 1124.
 DR GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR000058; Interleukin_10.
 DR ProDom; PDD03687; Interleukin_10; 1.
 DR SMART; SM01188; IL10_1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine.
 SQ SEQUENCE 220 AA; 2516 MW; 5B776C8612AC909D CRC64;

Query Match 24.4%; Score 222; DB 2; Length 220;
 Best Local Similarity 34.4%; Pred. No. 2.6e-13; DB 2;
 Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

Ov 17 LLMPPSTGIL-KLNLGSC-VIATNLQIIRNGFSDIRGSVQAKGNDIDIRLRTESLOPDKPANRCLLHR 73

Db 55 LLWNQVPGLEGGOFPRFGSCQTVGWLWEAFWTFVKTWQTPDDITTSIRLL-KPQVIRN 113

RT "Comparative genomic analysis reveals independent expansion of a
 lineage-specific gene family in vertebrates: The class II cytokine
 receptors and their ligands in mammals and fish.";

RT BMC Genomics 4:29-29 (2003);
 RL EMBL; AY294558; AY57416.1; -; mRNA.
 DR EMBL; AY294558; AY57416.1; -; mRNA.
 DR GO:00005615; C:extracellular space; IEA.
 DR GO:0005125; F:cytokine activity; IEA.
 DR GO:0006355; F:immune response; IEA.
 DR InterPro; IPR01251; Cytokine_4_hlx.
 DR InterPro; IPR00098; Interleukin_10.
 DR Pfam; PF00726; IL10_1.
 DR ProDom; PDD03687; Interleukin_10; 1.
 DR SMART; SM00188; IL10_1.
 DR SEQUENCE 175 AA; 1983 MW; DE6FA67B0038B034 CRC64;

RESULT 9

Q25S4 MOUSE

ID Q25S4_MOUSE PRELIMINARY; PRT; 181 AA.

AC Q25S4;

DT 01-DEC-2001 (Tremblel. 19, Created)
 DT 01-MAR-2004 (Tremblel. 26, Last annotation update)
 DB Melanoma differentiation associated gene-7.

GN Name=IL24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Eutheria; Bivalentoglii; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1];
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvJ;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL: AP235006; AAK5290_1; -; mRNA.
 DR ENSEMBL: ENSG000026420; Mus musculus.
 DR MG1: 2135548; IL24.
 DR GO: GO-0016515; C:extracellular space; TAS.
 DR InterPro: IPR00098; Interleukin_10.
 DR ProDom: PD003687; Interleukin_10; 1.
 DR SMART: SM00188; IL10; 1.
 DR PROSITE: PS00520; INTERLEUKIN_10; 1.
 KW CYTOKINE.
 SQ 181 AA; 20812 MW; 05CA43872D53D555 CRC64;
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 Best Local Similarity 34.4%; Pred. No. 3-2e-13;
 Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;
 QV 17 LLWNPSTGK-KTUNLGLC-VIATNQELRNGSDIROSVAQKDGNDITRRTESQD 73
 16 LLWNQVPGLEQFQRSGQCVTGIVVLPLEMFAWTVKQVYQDITRSIRL-KPQLRN 74
 Db 74 TKPANRCCUHLRHLVYLDRVPKQQT-PDHVILRKISSLANSPLTIDKDLRCHAHMT 131
 QY 75 VSGAESCYHLAHSILKFYNTVFKYHSLKAFKYTLRSFTLANNFIVIMSQGPKNSM 134
 Db 132 CHCCEAMKXYSQTLSHFKEKLEPOAVVKGALGENDILQME 174
 135 LPSESAAHORPLFRRAFQKQDTEVALVYGAFFEVLDILTWQK 177
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 IL24_HUMAN STANDARD; PRT; 206 AA.
 ID II24_HUMAN STANDARD; PRT; 206 AA.
 AC Q13007; Q96K4;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-MAY-2005 (Rel. 35, Last annotation update)
 DT 01-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-24 precursor (suppression of tumorigenicity 16 protein)
 DE (Melanoma differentiation-associated protein 7) (MDA-7).
 GN Name=IL24; Synonyms=MDA7, ST16;
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 RN [1]
 RP NCBITaxonID=9606;
 RN TISSUE=Melanoma;
 RX MEDLINE-9512699; PubMed=8545104;
 RA Jiang H., Lin J.J., Su Z.-Z., Goldstein N.I., Fisher P.B.;
 RT "Subtraction hybridization identifies a novel melanoma differentiation
 associated gene, mda-7, modulated during human melanoma
 differentiation, growth and progression.";
 RT Oncogene 11:2477-2486(1995).
 RN [2]
 RP NUCLEOTIDE_SEQUENCE.
 RA Peat J., Kube D., Eskdale J., Jueliger S., Gallagher G.;
 RT "The human mda-7 gene";
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE_SEQUENCE, AND VARIANT HIS-124.
 RC TISSUE= fibroblast;
 RA Madireddi M.T., Lin J., Su Z.-Z., Shay J.W., Huberman E., Fisher P.B.;
 RT "Genomic structure, chromosomal localization and expression of
 melanoma differentiation associated gene-7 (mda-7): potential
 relationship with cellular senescence";
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE_SEQUENCE [GENOMIC DNA], AND VARIANTS HIS-124; ARG-125 AND
 RP IEF-131.
 RA Rieder M.J., Armeal T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs: NHBL_Ht6682 program for genomic applications, UW-
 RT FHcrc, Seattle, WA (URL: http://pga.gs.washington.edu).";
 KW Polymorphism; Signal.

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE_SEQUENCE [LARGE SCALE RNA].
 RC TISSUE=Lung;
 RX MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grobe L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemnon C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Blatcknko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquai Lano N.A., Peters G.J., Abramson R.D., Mullally S.J.,
 RA Bosack S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Mozyk D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Slepchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S., Krzywinski M.I., Skalski U., Smailus D.E.,
 RA Schinner A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP PROTEIN_SEQUENCE_OF_52-66; PubMed=15340161; DOI=10.1101/pb.04682504;
 RX Zhang Z., Hanzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824 (2004).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=9826712; PubMed=9826712; DOI=10.1073/pnas.95.24.14400;
 RA Su Z.-Z., Madireddi M.T., Lin J.J., Young C.S.H., Kitada S.,
 RA Reed J.C., Goldstein N.I., Fisher P.B.;
 RT "The cancer growth suppressor gene mda-7 selectively induces apoptosis
 in human breast cancer cells and inhibits tumor growth in nude mice";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:14400-14405 (1998).
 CC CC and may contribute to terminal cell differentiation. May also
 CC CC function as a negative regulator of melanoma progression.
 CC CC Formation in vivo in nude mice. They found that it selectively
 CC CC induces apoptosis in human breast cancer cells.
 CC CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC CC -1- TISSUE_SPECIFICITY: Up-regulated in melanoma cells induced to
 CC CC terminally differentiate.
 CC CC -1- SIMILARITY: Belongs to the IL-10 family.
 CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC CC the European Bioinformatics Institute. There are no restrictions on its
 CC CC use as long as its content is in no way modified and this statement is
 CC CC removed.
 CC CC -----
 DR EMBL: U16261; AAQ91780_1; -; mRNA.
 DR EMBL: AR27616; ANG41401_1; -; Genomic_DNA.
 DR EMBL: AR235005; AAK5289_1; -; Genomic_DNA.
 DR EMBL: AV06231; AAL34146_1; -; Genomic_DNA.
 DR EMBL: BC00981; AAH0981_1; -; mRNA.
 DR ENSEMBL: ENSG0000162892; Homo sapiens.
 DR HGNC: HGNC:11346; IL24.
 DR H-InvDB: HIX0001532; -.
 DR MIM: 604136; -.
 DR GO: 0006215; P:apoptosis; TAS.
 DR InterPro: IPR01251; Cytokine_4_helix.
 DR InterPro: IPR00098; Interleukin_10.
 DR ProDom: PD003687; Interleukin_10; 1.
 DR SMART: SM00188; IL10; 1.
 DR PROSITE: PS00520; INTERLEUKIN_10; 1.
 KW Apoptosis; Cytokine; Direct protein sequencing; Glycoprotein;

DE	OS	Rattus norvegicus (Rat).
OC	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rattus.
OC	OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
DR	NCBI_TaxID=10116;	
RN	[1]	NUCLEOTIDE SEQUENCE.
RC	STRAIN=Sprague-Dawley;	
RX	MEDLINE=99308986; PubMed=103181256;	
RX	DOI=10.1002/(SICI)1097-4644(19990701)74:1<1::AID-JCB1>3.3.CO;2-D;	
RA	Soo C., Shaw W.W., Preymiller E., Longaker M.T., Bertolami C.N., Chiu R., Tieu A., Ting K.;	
RA	"Cutaneous rat wounds express c9a, a novel gene with homology to the human melanoma differentiation associated gene, mda-7.";	
RT	J. Cell. Biochem. 74:1-10(1999).	
CC	-1--SUBCELLULAR LOCATION: Secreted (By similarity).	
EMBL	AF004774; AAB69171.1; -; mRNA.	
DR	GO; GO_0005576; C:extracellular region; IEA.	
DR	GO; GO_0005125; P:cytokine activity; IEA.	
DR	GO_0006555; P:immune response; IEA.	
DR	InterPro; IPR000998; Interleukin_10.	
DR	ProDom; PDD03687; Interleukin_10.	
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QY	90 YLDRVKYQVQTP--DHYTURKISSLANSLTIKKDRLCHAMHTCHCREAMKYSQILS 147	
DB	93 YLNPFVQHNSKTVRKVFKVLSFSTLANNFLVIMSKLQPSKRDNDLPLSDSARRFLFHR 152	
QY	148 HPEKLEPQAVVKGELDILLQWME 173	
DB	153 TPKQDIEVALAKAFGEVUDILLAMQ 178	
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DT	25-OCT-2004 (TREMBLrel. 28, Created)	
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)	
DR	Interleukin-10.	
RN	[1]	NUCLEOTIDE SEQUENCE.
RA	Rothwell L., Young J., Zoorob R., Whittaker C.A., Hesketh P., Archer A., Smith A.L., Kaiser P.,	
RA	"Cloning and Characterization of Chicken IL-10 and Its Role in the Immune Response to Elmerita maxima.";	
RL	J. Immunol. 173:2675-2682(2004).	
DR	EMBL; AU621614; CAF21271.1; -; Genomic DNA.	
DR	GO; GO_0005576; C:extracellular region; IEA.	
DR	GO; GO_0005125; P:cytokine activity; IEA.	
DR	GO; GO_0006555; P:immune response; IEA.	
DR	InterPro; IPR012351; Cytokine_4_helix.	
DR	InterPro; IPR000998; Interleukin_10.	
DR	PFam; PF00226; IL10; 1.	
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DR	ProDom; PDD03687; Interleukin_10.	
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QY	60 IDIRLIRRTESTDQPTKPNRCCRLRHLLRVLDRVKYQVOTPDHYTURKISSLANSFLI 119	
DB	58 LNIQHLL-SSLLDUFKGTGPGCQSYSEMLRPFYDVLPRAMQTSSTSHQSMGDLGMLGL 116	
QY	120 KDLRLCHAMHTCHCGERAMKYSQILSHPEKLEPQAVVKGELDILLQWME 174	
DB	117 KATIRRCHRFFTC--EKRSKAIKOIKETPEKQD-ENGIYKAMGEFDIPINYIE 167	

Tue Jan 3 11:53:23 2006

us-10-789-251-2.rup

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Job time : 230 secs

GenCore version 5.1.6
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11: gb_sy:
12: gb_un:
13: gb_vl:
14: gb_htg:
15: gb_pl:
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ALIGNMENTS

RESULT 1
BB087297
LOCUS BB087297 926 bp DNA linear PAT 27-AUG-2002
DEFINITION Mammalian cytokine-like polypeptide-10.
ACCESSION BB087297
VERSION BB087297.1 GI:2262907
KEYWORDS JP 2001524313/A/1
SOURCE Homo sapiens (human)
ORGANISM Homo Sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo;
REFERENCE 1 (bases 1 to 926)
AUTHORS Conklin, D. C., Halderman, B. A. and Grossmann, A.
TITLE Mammalian cytokine-like Polypeptide-10
JOURNAL Patent: JP 2001524313-A 1 04-DEC-2001;
REFERENCE ZYMOGENETICS INC
COMMENT OS Homo sapiens (human)
COMMENT OS Homo sapiens (human)
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COMMENT PN JP 2001524313-A/1
COMMENT PN JP 2001524313-A/1
COMMENT PD 04-DEC-2001
COMMENT PD 04-DEC-2001
COMMENT PR 25-NOV-1998 JP 2000522345
COMMENT PR 26-NOV-1997 US 08/919156
COMMENT PI DARIBILL C CONKLIN BETTY A HALDEMAN ANGELIKA GROSSMANN PC
C12N15/00, A01K67/027, A61K38/00, A61K48/00, A61P1/02, A61P1/00, PC
A61P17/00, A61P17/05, A61P37/02, A61P43/00, C07K14/52, C07K16/24, C07K16/26, PC
C12N15/00, A61P37/02, A61P43/00, C07K14/52, C07K16/24, C07K16/26, CS109174 Sequence

PC A61K37/02
 CC Mammalian cytokine-like polypeptide-10
 FH Location/Qualifiers
 KEY
 FT
 CDS
 FEATURES
 SOURCE
 ORIGIN
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US-10-789-251-26 (1-144) x BD087297 (1-926)

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 261 GACACAAACCTGCGATCAGTCGCTCTGGCCATTGTCAAGACTCTATGGAC 320
 QY 61 ArgValPheIleAspIleArgIleLeuGlnGlyIleSerIle 80
 Db 321 AGGTTTAAACTTACAGACCCGTTGCAATATCTCCGAAGTCAGACGCTC 380
 QY 81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuGlyIleSerIle 100
 Db 381 GCCATTCCTTCTTACATCAAGAGGACTCTGGCTCTGTCATGCCACATCAC 440
 QY 101 HisCysGlyIleGluIleAlaMetLysTyrSerGlnIleLeuSerHisPheGluIle 120
 441 CATGGGGAGGAGAGCAATGAGAACTACGCCAGATTCGACTCTGAAAGCTG 500
 Db 121 GluProGlnAlaIleValValIleAlaLeuGlyIleLeuGlnIleLeu 140
 QY 501 GAACCTGGCAGGAGCTGGAGGCTTGGGAACTAGCAATCTTGCAATGGTG 560
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RESULT 2
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 LOCUS CQ818183
 DEFINITION Sequence 1 from Patent EP1424393.
 ACCESSION CQ818183
 VERSION CQ818183.1
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE 1. Conklin, D.C., Haldeman, B.A. and Grossmann, A.
 AUTHORS
 TITLE Mammalian cytokine-like polypeptide-10
 JOURNAL Patent: EP 1424393-A 1 02-JUN-2004;
 ZymoGenetics Inc (US)
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 1. .926
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 Best Local Similarity: 100.00%
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 ALGELDILLOMEETE"

US-10-789-251-26 (1-144) x CQ818183 (1-926)

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 QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuGlnGlySerLeuGln 40
 Db 201 GTGCGAGCCAGATGAGATCACATAGAATCTTGGAGACTGATCTTGCA 260
 QY 41 AspThrIleProAlaAspIleArgIleLeuGlnGlyIleSerIle 80
 Db 321 AGGTTTAAACTTACAGACCCGTTGCAATATCTCCGAAGTCAGACGCTC 380
 QY 81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuGlyIleSerIle 100
 Db 381 GCCATTCCTTCTTACATCAAGAGGACTCTGGCTCTGTCATGCCACATCAC 440
 QY 101 HisCysGlyIleGluIleAlaMetLysTyrSerGlnIleLeuSerHisPheGluIle 120
 441 CATGGGGAGGAGAGCAATGAGAACTACGCCAGATTCGACTCTGAAAGCTG 500
 Db 121 GluProGlnAlaIleValValIleAlaLeuGlyIleLeuGlnIleLeu 140
 QY 501 GAACCTGGCAGGAGCTGGAGGCTTGGGAACTAGCAATCTTGCAATGGTG 560
 Db 141 GluGluThrIle 144
 561 GAGGAGACGAA 572

RESULT 3
 CS109174
 LOCUS CS109174
 DEFINITION Sequence 1 from Patent WO2005052001.
 ACCESSION CS109174
 VERSION CS109174.1
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE 1. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Hominidae; Homo.
 AUTHORS Xu, W., Kindsyvogel, W.R., Chen, Z., Hughes, S.D., Chandrasekher, Y.A., Dillon, S.R., Lehner, J.M., Siedak, A.W., Sivakumar, P.V. and Moore, M.D.
 TITLE Anti-IL-20 receptor antibodies and binding partners and methods of using in inflammation

JOURNAL		Patent: WO 200502001-A 1 09-JUN-2005;	
FEATURES		ZymoGenetics, Inc. (US)	
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ORIGIN		ORIGIN	
Alignment Scores:		Alignment Scores:	
Pred. No.: 3.226-72		Length: 926	
Score: 753.00		Matches: 144	
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DB 201 GTGCGAGCCAGCTGGAATGATGATGTCGCTCCTGCGCATTCAGGAGCTATCTGCA 260		DB 201 GTGCGAGCCAGCTGGAATGATGATGTCGCTCCTGCGCATTCAGGAGCTATCTGCA 260	
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RESULT 4		RESULT 5	
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DEFINITION ACCESSION VERSION		DEFINITION ACCESSION VERSION	
SOURCE ORGANISM		SOURCE ORGANISM	
. Homo sapiens (human)		. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Nammalia; Buteria; Buarchoptoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
SOURCE		Unknown.	

ORGANISM	Unknown	Unclassified
REFERENCE	1 (bases 1 to 926)	1 (bases 1 to 926)
AUTHORS	Conklin, D.C. and Haldeman, B.A.	Conklin, D.C. and Haldeman, B.A.
TITLE	Mammalian cytokine-like polypeptide-10	Interleukin 20: discovery, receptor identification, and role in epidermal function
JOURNAL	Patent: US 6576743 A 1 10-JUN-2003; ZymoGenetics, Inc.; Seattle, WA	Cell 1104 (1), 9-19 (2001)
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Best Local Similarity:	100.00%	Mismatches: 0
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Qy	21 ValGlnAlaLysIleAspGlyAsnIleAspIleArgIleLeuArgArgGlySer 40	source
Db	201 GTCGAGCCAAAGTTGGAACTTGACATCAGAATCTTGGAGGACTGAGCTTGCAA 260	REFERENCE
Qy	41 AspThrIleProIleAspArgCysCysIleLeuArgIleLeuArgIleLeuArgIleLeuAsp 60	AUTHORS
Db	261 GACACAAAGCTCGGAACTGATCGTGTGCTGCCCTGCGCCATTGCTAGACTCTTGAC 320	JOURNAL
Qy	61 ArgValPheLysIleAsnTyrGlnIleProAspHisTyrThrLeuArgIleLeuSerSerIleu 80	Submitted (12-JAN-2000) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, Wa. 98102, USA
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AF224266		ORIGIN
LOCUS	AF224266	Alignment Scores:
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ACCESSION		Score: 753.00
VERSION		Percent Similarity: 100.00%
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Qy	61 ArgValPheLysIleAsnTyrGlnIleProAspHisTyrThrLeuArgIleLeuSerSerIleu 80	DB: 8
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KEYWORDS	MGC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	
AUTHORS	
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Collins FS, Wagner L, Shrem CM, Schulz GD, Altshul SF, Zeeberg	/translation="MKASIAFSLSAFAFLWTFSTGLTTLNLGSCTVATNLOBIRN
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SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,	
Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,	
Villalon DK, Muzny DM, Sodergren BJ, Lu X, Gibbs RA, Fahey J,	
Heltor B, Kettman M, Rodriguez S, Sanchez A, Whiting M,	
Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,	
Tuchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,	
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CONSRTRM	
TITLE	Generation and initial analysis of more than 15,000 full-length
JOURNAL	human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLISHED	12/27/93
REFERENCE	2 (bases 1 to 531)
AUTHORS	
Director MGC Project.	
COMMENT	Director Submission
JOURNAL	Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer	
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
USA	
NIH-MGC Project help desk: http://mgc.nci.nih.gov	
EMail: cggbs-@email.nih.gov	
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VERSION	BC069523.1
KEYWORDS	GI:47479431
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
Hominidae; Homo.	
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AUTHORS	
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Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klaunser RD,	
Collins FS, Wagner L, Shrem CM, Schulz GD, Altshul SF, Zeeberg	
B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,	
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Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,	
Villalon DK, Muzny DM, Sodergren BJ, Lu X, Gibbs RA, Fahey J,	

CONSRM	TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	1	CrystallieAelamrAsleugingIngleuleArgAsnGlyPhosserAspLeuArgLyser	20
JOURNAL	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	97	TGTGTGATGCGCACAACTTCAGGAAATACGAATGGATTCTGAGCATACGGGACT	156
PUBMED	PUBMED	12477932	21	ValGlnAlaLysAspGlyAsnLeaspIleAspIleAspIleLeuargargArgThrGluGln	40
AUTHORS	AUTHORS	2 (bases 1 to 531)	2	GACACAAGCTCGGAATCGATCTGCTCCCTGGCCATTGCTAAAGCT	276
REMARK	REMARK	Director MGC Project.	217	GAGGAAAGCTGGCAAGCTGAGGAGCTAGCTTGAA	276
COMMENT	COMMENT	Direct Submission	217	GATGAAAGCTGGCAAGCTGAGGAGCTAGCTTGAA	276
TITLE	TITLE	Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	41	AspThrIysProIlaAsnArgCysCysLeuIaargHsIleLeuArgLeuArgThrLeuasp	60
JOURNAL	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	41	ValGlnAlaLysAspGlyAsnLeaspIleAspIleAspIleLeuargargArgThrGluGln	40
PUBMED	PUBMED	12477932	21	GACACAAGCTCGGAATCGATCTGCTCCCTGGCCATTGCTAAAGCT	276
DB	DB	NIH-MGC Project URL: http://mgc.ncbi.nih.gov	217	GAGGAAAGCTGGCAAGCTGAGGAGCTAGCTTGAA	276
CONTACT	CONTACT	Direct Submission	217	GATGAAAGCTGGCAAGCTGAGGAGCTAGCTTGAA	276
EMAIL	EMAIL	cgabbs-r@mail.nih.gov	217	GATGAAAGCTGGCAAGCTGAGGAGCTAGCTTGAA	276
TISSUE	TISSUE	Procurement: Baylor Human Genome Sequencing Center	61	ArgValPheLysSerThrGlnThrProAspPheAspTyrThrLeuargIleLeuSerSerIeu	80
FEATURES	FEATURES	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	277	GGGTGTTAAACTACCAACCCCTGACCATTA	336
SOURCE	SOURCE	CDNA Library Preparation: Baylor Human Genome Sequencing Center	81	AlaAsnSerPheLeuThrIleLysIleLysIleLeuGlyCysHisAlaIleMetThrCys	100
CDNA	CDNA	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUMI)	397	CATGTGGGAGGAGCATGAGAAATACACGCCAGATTCCTGAGTCAC	456
LIBRARY	LIBRARY	DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center	121	GluProGlnAlaIleValValysAlaIleGlyGluLeuAspIleLeuLeuGluIntrpMet	140
CONTACT	CONTACT	Center code: BCM-HGSC	457	GAACCTCAGGCAAGCTGTTGCGGAACTAGAGATTCCTCTGCGATGGATG	516
WEB SITE	WEB SITE	Web site: http://www.hgsc.bcm.tmc.edu/cdna/	QY	141 GluGluGluGluGlu 144	517
CONTACT	CONTACT	Contact: P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lousegod, H., Kowles, C.R., Sned, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	Db	517 GAGGAGAGAGA 528	517
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ORIGIN	ORIGIN		Db		
ALIGNMENT	ALIGNMENT		Db		
SCORE	SCORE		Db		
PRED. NO.	PRED. NO.	4.73e-72	Db		
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JOURNAL	JOURNAL	Mammalian Gene Collection Program Team	Db		
PUBMED	PUBMED	Smallius DR, Schnerch A, Schein JE, Jones SJ and Marra MA.	Db		
REFERENCE	REFERENCE	Mammalian Gene Collection, Team	Db		
AUTHORS	AUTHORS	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	Db		
JOURNAL	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	Db		
PUBMED	PUBMED	12477932	Db		
REFERENCE	REFERENCE	2 (bases 1 to 531)	Db		
AUTHORS	AUTHORS	Director MGC Project.	Db		
JOURNAL	JOURNAL	Direct Submission	Db		
CONSRM	CONSRM	Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	Db		
JOURNAL	JOURNAL	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	Db		
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REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk

Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center Code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cDNA/>
Contact: amg@bcm.tmc.edu
Gunnarsson, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsaged, H.,
Kowalski, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRBR Plate: 1 Row: b Column: 3.
Location/Qualifiers
1. 531

Search completed: December 28, 2005, 12:45:48
Job time : 2950 secs

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  ALGELDILQWMEETE"
  CDS

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Percent Similarity:		Conservative:	1
Best Local Similarity:	99.31%	Mismatches:	0
Query Match:	99.47%	Indels:	0
		Gaps:	0

ORIGIN

Qy	1	CysValIleAlaThrAsnLeuIleGlnGluLeuArgAlaGlyPheSerAspIleArgGlySer	20
Db	97	TGTTGATGCCAACACCTCAGGAAATCGAATGGATTTCAGATACGGGGCACT	156
Qy	21	ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln	40
Db	157	GTGCAAGCCAAAGATGGAAACATTCACATCGAACTTAAGGAGACTGAGCTGACTTGTCAA	216
Qy	41	AspThrIleProAlaAsnAlaGlyCysLeuLeuLeuAspGlyHistidineLeuArgLeuAsp	60
Db	217	GACAAAGGCTGCGRATCGATGCTGCCTCTGCGCCATTGTGCTAGACTCTATGGAC	276
Qy	61	ArgValAlpheIysAsnTyrglnIleProAspHisTyglnIleLeuArgLysIleSerSerLeu	80
Db	277	AGGTTTAAACTACAGACCCCTGACCATTTACTCTCGGAGATCAGCGCCTC	336
Qy	81	AlaAsnSerPheLeuThrIleLysIleAspIleLeuIleLeuCysHialaLahisMetThrCys	100

PR 12-AUG-2002; 2002JP-00234880.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 2004-320878/30.
 XX
 PR P-PSDB; ADM95041.
 PT Agent useful for prevention and/or treatment of colon cancer, comprises
 PT interleukin 20 (IL-20), IL-20 receptor alpha chain, IL-20 receptor beta
 PT chain.
 XX
 PS Disclosure; SEQ ID NO 10; 50pp; Japanese.
 XX
 CC This invention relates to a novel agent for prevention and/or treatment
 CC of colon cancer, comprising of the interleukin 20 (IL-20) receptor alpha
 CC chain, its partial peptide or salt. The invention may be useful for the
 CC development of compounds with a cytotoxic activity. The invention is
 CC useful for preventing and/or treating colon cancer. A diagnostic agent is
 CC salt or its peptide, compounds that have altered binding property towards
 CC them can be efficiently screened. The present sequence is that of a gene
 CC which encodes the human interleukin-20 protein and which is related to
 the invention.
 XX
 SQ Sequence 528 BP; 148 A; 129 C; 122 G; 129 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5.13e-87 Length: 528
 Score: 753.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 12 Indels: 0
 DB: Gaps: 0
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 DB 97 TGTGTGATGCCACAACTTCAGAAATAGGAAATGGATTCTGACATGGGAGT 156
 QY 21 ValGlnAlaLysAspGlyAsnAspIleAspIleArgIleLeuArgArgGlyGluSerLeuGln 40
 DB 157 GTGCAAGCCAAGATGGAAATGAGATCTAGAGATCTTGGAGGACTGAGCTTGCA 216
 QY 41 AspThrIleProAlaAsnArgCysCysteoleuArgIleLeuArgIleLeuArgIleLeuAsp 60
 DB 217 GACCAAGCTCGCAATGATGATCTGCCCTCTCGCCATTCTGACTATCTGAC 276
 QY 61 ArgValIlePhelLysAsnTyrGlnIleProAspHisIleTyrThrIleLeuArgIleLeuSerSerIle 80
 DB 277 AGGTTATTTAAACTACCGACCCCTGACGATTAATCTCCGAAAGATCAGACGCTC 336
 QY 81 AlaAsnSerPheIleThrIleIleIleAspIleLeuArgCysIleAlaHisMetThrCys 100
 DB 337 GCCATTCCTTCTTACATCAAGAGGACCTGGCTGTCATGCCACAGACATGC 396
 QY 101 HisCysGlyGluIleAlaLeuIleValLysTyrSerGlnIleLeuSerIlePhelGluIleIle 120
 DB 397 CATTTGGGGAGGAGCAATGAGAAATACCGAGATCTGAGTCATCTGAAAGCTG 456
 QY 121 GluProGlnIleAlaValValIleAlaIleAspIleLeuLeuGlnIleAsp 140
 DB 457 GACCTCAAGCAGCAGCTGCTGAGCTTGGGAACTAGACAATCTCTGCATGGATG 516
 QY 141 GluGluIleGlu 144
 DB 517 GAGGGAGCAGAA 528
 RESULT 2
 ADV42800 ID ADV42800 standard; cDNA: 531 BP.
 XX ADV42800; AC

XX 10-MAR-2005 (first entry)
 DT
 XX DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 428.
 XX KW microarray; psychoneuroendocrinimmune; chronic fatigue; inflammation;
 KW non-insulin dependent diabetes; allergy; immune disorder; infection; expressed sequence tag; ss.
 KW cancer; neoplasm; expressed sequence tag; ss.
 OS Homo sapiens.
 XX PN WO2004108899-A2.
 XX RD 16-DEC-2004.
 XX PR 04-JUN-2004; 2004WO-US017686.
 XX PR 04-JUN-2003; 2003US-0475915P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Nicholson A, Vernon SD;
 DR WPI; 2005-031682/03.
 XX PN New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a condition associated with PNI activity, e.g., inflammatory or infectious diseases.
 XX PS Claim 1; SEQ ID NO 428; 254pp; English.
 CC The invention relates to a new microarray which comprises probes for genes involved in psychoneuroendocrinimmune (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as CFS, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a psychoneuroendocrinimmune gene expressed sequence tag. Note the specification mentions SEQ ID NO of up to 3314 but only sequences up to SEQ ID NO 1829 are provided.
 XX SQ Sequence 531 BP; 149 A; 129 C; 123 G; 130 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5.18e-87 Length: 531
 Score: 753.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 14 Indels: 0
 DB: Gaps: 0
 US-10-789-251-26 (1-144) x ADV42800 (1-531)
 QY 1 CysValIleAlaThrAsnLeuGlnGluLeuArgAsnGlyPheSerAspIleArgGlySer 20
 DB 97 TGTGTGATGCCACAACTTCAGAAATGGATTCTGACATGGGAGT 156
 QY 21 ValGlnAlaLysAspGlyAsnAspIleAspIleArgIleLeuArgArgGlyGluSerLeuGln 40
 DB 157 GTGCAAGCCAAGATGGAAATGAGATCTAGAGATCTTGGAGGACTGAGCTTGCA 216
 QY 41 AspThrIleProAlaAsnArgCysCysteoleuArgIleLeuArgIleLeuArgIleLeuAsp 60
 DB 217 GACCAAGCTCGCAATGATGATCTGCCCTCTCGCCATTCTGACTATCTGAC 276
 QY 61 ArgValIlePhelLysAsnTyrGlnIleProAspHisIleTyrThrIleLeuArgIleLeuSerSerIle 80
 DB 337 GCCATTCCTTCTTACATCAAGAGGACCTGGCTGTCATGCCACAGACATGC 396

be therapeutically useful in the regeneration of the gastrointestinal tract or oral cavity, as well as in the treatment of asthma, and other diseases of the tracheobronchial tract such as bronchitis. Cytol0 polypeptides may also be useful to promote wound healing, and to increase platelet count, e.g., in cancer patients who experience thrombocytopenia.

PT /*tag= c
 XX
 PN WO2003051384-A1.
 XX
 PD 26-JUN-2003.
 XX
 PP 17-DEC-2002; 2002WO-US040309.
 XX
 PR 17-DEC-2001; 2001US-0341783P.
 XX
 PA (LUNN/) LUNN P G.
 XX
 PT Chandrasekher YA, McKernan PA;
 XX
 WPI; 2003-69114/53.
 DR P-PSDB; ABRO2464.
 XX
 PT Inhibiting the growth and/or proliferation of cervical cancer cells, useful for treating cervical cancer or human papilloma virus infection, comprises bringing Interleukin-20 (IL-20) into contact with the cervical cancer cells.
 XX
 PS Disclosure; Page 11-12; 26pp; English.
 XX
 CC The present sequence is that of a polynucleotide encoding human interleukin-20 (IL-20), including the signal sequence. The invention relates to the use of IL-20 for treating cervical cancer or cells infected with human papilloma virus. IL-20 can be administered alone or in conjunction with radiation or chemotherapeutic agents or surgical excision of the involved cells or lesions
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 Alignment Scores:
 Pred. No.: 1.17e-86 Length: 926
 Score: 751.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps:
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 DB 201 GTGCAAGGCCAAAGATGGACATGACTAGATCTAGGGAGATGAGCTTGGAA 260
 OY 41 AspThrLysProLysAspArgCysCysLeuLeuArgLysLeuArgLysLeuAsp 60
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 OY 61 ArgValPheLysAlaArgLysGlnThrProAlaPheIleSerSerIle 80
 DB 321 AGGGATTTAAAGTACCAAGACCCCTGACCATATACTCTGGAGATCAGAGCTC 380
 OY 81 AlanAsnSerPheLeuThrLysLysAspLeuArgLysCysBishAlaHisMetThrCys 100
 DB 381 GCCATTCTTCCTTCTACATCAGAGGACCTGGCTGTCATGCCACATGACATGC 440
 OY 101 HisCysGlyLysGluLysAlaMetLysLysTyrSerGlnLeuSerHisPheGluLeu 120
 DB 441 CATTGTGGGGAGGAGGAGCATGAGAAATGAGCAGATCTGACTTGTGAAAGCTG 500
 OY 121 GluProGlnAlaAlaValValValAlaLeuGlyGluLeuAspIleLeuGlnTrpMet 140
 DB 501 GAACTCTAGGAGCAGCTGCTGAGGCTTGGGCAACTAGACATCTCTGCAATG 560
 OY 141 GluGluLysGlu 144

Db 561 GAGGAGCAGAA 572
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 RESULT 5
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 DT 15-JAN-2004 (first entry)
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 DE Human cytokine-like polypeptide-10 (Zcyto10) cDNA.
 XX
 KW Human; cytokine-like polypeptide-10; Zcyto10; therapy; thrombocytopaenia;
 KW autoimmune disease; insulin-dependent diabetes mellitus; immune response;
 KW rheumatoid arthritis; multiple sclerosis; infection; radiation therapy;
 KW asthma; bronchitis; wound healing; Periodontal disease; antiinflammatory;
 KW psoriasis; eczema; dry skin; oral cavity; muscle atrophy; haemostatic;
 KW cancer; vulnerability; chromosome 1; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/qualifiers
 PT CDS 45. .575
 PT /*tag= a
 PT sig_peptide 45. .116
 PT mat_peptide /*tag= b
 PT /*tag= c
 PT /*product= "Mature human Zcyto10"
 XX
 PN US6576743-B1.
 XX
 PD 10-JUN-2003.
 XX
 PR 17-MAY-1999; 99US-00313458.
 XX
 PR 26-NOV-1997; 97US-0066597P.
 PR 25-NOV-1998; 98US-00199586.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PT Conklin DC, Haldeman BA;
 XX
 DR WPI; 2003-799824/75.
 P-PSDB; ABW00889.
 XX
 PT Novel human cytokine-like polypeptide-10, Zcyto10, useful for treating insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple sclerosis, asthma, psoriasis and inhibiting cancer cell growth.
 XX
 PS Disclosure; Col 29-30; Opp; English.
 XX
 CC The invention relates to an isolated human cytokine-like polypeptide-10 (Zcyto10) polypeptide. Zcyto10 is useful for prevention or treatment of conditions characterised by improper cell proliferation, cell differentiation or cytokine production. Zcyto10 is useful for treating autoimmune diseases such as insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple sclerosis, etc., by inhibiting cellular immune response. The invention is useful for inhibiting cancer cell growth or proliferation, for stimulating immune system to combat microbial or viral infections, for increasing platelet production, and thus useful in cancer patients who experience thrombocytopaenia due to cancer therapy or radiation therapy. Zcyto10 is useful in tracheobronchial-specific or tracheobronchial-specific applications, such as in the maintenance or would repair of the tracheobronchial epithelium or cells underlying the same, in regulating mucous production or mucociliary clearance of debris or in treatment of asthma, bronchitis or other diseases of the tracheobronchial tract. Zcyto10 may also enhance wound healing and promote regeneration of affected tissues which may be especially useful in the treatment of periodontal disease. Zcyto10 can be used to treat skin conditions such as psoriasis, eczema and dry skin in general. Zcyto10 is useful for regenerating gastrointestinal tract or

FT mat_peptide 117. .572
FT /*tag= C
FT /product= "Human mature Zcyt610 protein"
FT

Alignment Scores: Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
 Pred. No.: 1.17e-85 Length: 926
 Score: 753.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

PN
XX
PD
18-SEP-2003.
XX
XX
15-APR-2003; 2003US-00413661.
PR
26-NOV-1997; 97US-0066597P.
PR
25-NOV-1998; 98US-0019586P.
PR
17-MAY-1999; 99US-0031345P.

Alignment:	Scores:
Fred. No.:	1.17e-86
Score:	753.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	10

Length:	926
Matches:	144
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

AC ADG46668;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human Zcyt010 DNA #1.
 XX
 KW cytokine-like polypeptide-10; Zcyt010; wound healing;
 KW platelet proliferation; wound repair; mucous production; asthma;
 KW bronchitis; tracheobronchial tract disease; periodontal disease;
 KW skin condition; psoriasis; eczema; dry skin; protein therapy; human;
 KW vulnerable; respiratory; antibronchitic; dental; dermatological; gene; ds
 XX
 OS Homo sapiens.

Key	Location/Qualifiers
FR	
FT	45. .575
FT	/*tgg= b
FT	/product= "Human Zcytolo protein"
FT	45. .116
FT	/*tgg= a
FT	
FT	
sig_peptide	

Qy 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
 CC (Zcyt010) proteins and their encoding polynucleotides. The invention is
 CC useful for treating conditions characterised by improper cell
 CC proliferation, cell differentiation or cytokine production, specifically
 CC for treating autoimmune diseases such as insulin dependent diabetes
 CC mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
 CC cancer cell growth. The invention is also used to stimulate the immune
 CC system, to enhance wound healing and promote regeneration of affected
 CC tissues, to increase platelet count and to treat asthma and skin
 CC conditions such as psoriasis, eczema and dry skin. The invention acts as
 CC an antidiabetic, neuroprotective, antirheumatic, antiarthritic, antiasthmatic and
 CC cytostatic, immunomodulant, pulmonary, antiasthmatic, antipsoriatic and
 CC dermatological agent. The invention is also used in gene therapy. The
 CC present sequence is human Zcyt010 longer form DNA.

RESULT 7

ADQ8066 standard; DNA; 926 BP.

XX ADQ8066;

XX AC

XX DT 07-OCT-2004 (first entry)

XX DE Human Zcyt010 longer form DNA.

XX KW Mammalian cytokine-like polypeptide-10; Zcyt010; cell proliferation;
 KW cell differentiation; cytokine production; autoimmune disease;
 KW insulin dependent diabetes mellitus; multiple sclerosis;
 KW rheumatoid arthritis; cancer; wound healing; tissue regeneration;
 KW platelet count; asthma; skin disease; psoriasis; eczema; dry skin;
 KW antidiabetic; neuroprotective; antiarthritic; cytostatic;
 KW immunomodulant; pulmonary; antipsoriatic; dermatological;
 KW gene therapy; human; gene; ds.

XX OS Homo sapiens.

XX PH

XX Key Location/Qualifiers

FT CDS

FT /tag= b 45..575

FT /product= "Human Zcyt010 protein"

FT sig_peptide 45..116

FT /tag= a 117..572

FT mat_peptide

FT /tag= C 141..575

FT CDS

FT /tag= d 141..575

FT /product= "Human Zcyt010 protein fragment"

FT /partial

FT /note= "No start codon"

XX US2004142428-A1.

XX PD 22-JUL-2004.

XX PP 27-FEB-2004; 2004US-00789129.

XX PR 26-NOV-1997; 97US-0066597P.

PR 25-NOV-1998; 98US-00199386.

PR 15-APR-2003; 2003US-00413661.

XX PA (ZYMO) ZYMOGENETICS INC.

XX Conklin DC, Haldeman BA;

XX WPI; 2004-552564/53; P-PSDB; ADQ8067, ADQ8077, ADQ8091.

XX PT New Zcyt010 polypeptides and polynucleotides, useful for treating
 PT autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple
 PT sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
 PT eczema). Disclosure; SEQ ID NO 1; 31pp; English.

XX

CC The present invention provides mammalian cytokine-like polypeptide-10
 CC (Zcyt010) proteins and their encoding polynucleotides. The invention is
 CC useful for treating conditions characterised by improper cell
 CC proliferation, cell differentiation or cytokine production, specifically
 CC for treating autoimmune diseases such as insulin dependent diabetes
 CC mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
 CC cancer cell growth. The invention is also used to stimulate the immune
 CC system, to enhance wound healing and promote regeneration of affected
 CC tissues, to increase platelet count and to treat asthma and skin
 CC conditions such as psoriasis, eczema and dry skin. The invention acts as
 CC an antidiabetic, neuroprotective, antirheumatic, antiarthritic, antiasthmatic and
 CC cytostatic, immunomodulant, pulmonary, antiasthmatic, antipsoriatic and
 CC dermatological agent. The invention is also used in gene therapy. The
 CC present sequence is human Zcyt010 longer form DNA.

XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

XX SQ

US-10-789-251-26 (1-144) x ADQ8066 (1-926)

Alignment Scores:

Pre. No.: 1.17e-66 Length: 926

Score: 753.00 Matches: 144

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0

DB: 201 GTCGACGCCAGATGCGACATGAGCTTCTGGAGCTGAGCTTCGAA 260

Qy 41 AspThrIysProAlaSerArgCysCysLeuLeuArgIleLeuArgLysLeuArg 60

DB 261 GACACAAGCCGCGAATGCGCTCTGCGCCATTGCTAACCTCTGAC 320

Qy 61 ArgValPhenylAsnTrpGlnThrProAspHisTyrThrLeuArgLysIleSerLeu 80

DB 321 AGGGTATTAAACTTACCAAGACGCCCTGACATTACTCTCGGGAGATCGACCTC 380

Qy 81 AlaAsnSerPhenylIleLysLysAspLeuArgLeuCysBisAlaHisMetThrCys 100

DB 381 GCCAATTCCTCTTCTACATCAGGACCTCCGGCTCTGCTCATGCCACTGACTGC 440

Qy 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheIleLeu 120

DB 441 CATTGCGGAGGAGGATGAGAATACAGCCAGTTCTGAGCTTCTGAAACCTG 500

Qy 121 GluProGlnAlaLalaValValAlaLeuGlyGluLeuAspLeuLeuLeuLysLeu 140

DB 501 GAACTCTGGCGAGCACTTGAGGCTTGGGAACTAGACATTCTGCAATGATG 560

Qy 141 GluGluThrGlu 144

DB 561 GAGGAGCAGAA 572

RESULT 8

ADR16327

XX ID ADR16327 standard; DNA; 926 BP.

XX AC ADR16327;

XX DT 21-OCT-2004 (first entry)

XX DE Human cytokine-like polypeptide-10 (Zcyt010) long form DNA.

XX KW Cytokine-like polypeptide-10; Zcyt010; therapy; asthma; infection;
 KW psoriasis; eczema; dry skin; wound healing; platelet proliferation;
 KW human; gene; ds.

XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 45. .575
 FT CD5 /*tag= b
 FT /*product= "Zcyto10 long form protein"
 FT 45. .116
 FT /*tag= a
 FT 117. .572
 FT /*tag= C
 FT /*product= "Nature Zcyto10 long form protein"
 XX US2004152878-A1.
 PN
 XX 05-AUG-2-2004.
 XX PR 27-FEB-2004; 2004US-00789958.
 XX PR 26-NOV-1997; 97US-0066597P.
 XX PR 25-NOV-1998; 98US-00199586.
 PR 15-APR-2-2003; 2003US-00413661.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PT Conklin DC, Haldeman BA;
 XX DR WPI; 2004-580197/56.
 DR P-PSDB; ADR16328, ADR16338.
 XX PT New isolated antibody that binds to a Zcyto10 polypeptide, useful for
 PT treating asthma, microbial or viral infections, and for promoting the
 PT healing of wounds, psoriasis, eczema or dry skin.
 XX Disclosure; SEQ ID NO 1; 32pp; English.
 CC The invention relates to novel cytokine-like polypeptide-10 (Zcyto10)
 CC polypeptides and polynucleotides. Zcyto10 Sequences are useful for
 CC treating asthma, microbial or viral infections, psoriasis, eczema or dry
 CC skin, for promoting the healing of wounds and for stimulating the
 CC proliferation of platelets. The present sequence is human Zcyto10 DNA.
 XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.17e-86 Length: 926
 Score: 753.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 13 Indels: 0
 DB: Gaps: 0
 US-10-789-251-26 (1-144) x ADR16327 (1-926)
 QY 1 CysValIleAlaThrAspIleGlnGluIleArgAsnGlyPheSerAspIleArgIleGlySer 20
 QY 141 TGTTGATGCCACAACTCTTCCAGGAAATGAGATTCTTGACATACGGGCGT 200
 QY 21 ValGlnAlaLysArgIleAspIleGlyLeuArgArgGlnGluSerLeuGln 40
 DB 201 GTGCCAAACCAAGATGAGAACATGACATAGCTTAAAGGAGCTGGCTTGCAA 260
 DB 201 AGGGTATTAAGAACTACAGACCCCTGACATTATACTCTCGGAGATGAGCA 380
 DB 41 AspThrLysProAlaAsnGlyCysCysLeuLeuLeuArgIleLeuLeuArgLeuTyrLeuP 60
 DB 261 GACACAAAGCCCTGGAAATGAGCTGGCTCCGGCCATTGCTAAGCTCTCTGGAC 320
 QY 61 ArgValPheLysArgTyrGlnThrProAspPheIstTyrThrLeuArgLysIleSerLeu 80
 QY 131 GGGTATTAAGAACTACAGACCCCTGACATTATACTCTCGGAGATGAGCA 380
 DB 81 AlaAsnSerPheLeuThrIleLeuLysArgLeuGlySerIleAlaLysMetThrCys 100
 DB 381 GCGATTCCTTCTTACCATCAAGAAACCTCGGCTCTGCTCATGCCACTGAGTC 440
 QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgIleSer 20
 QY 141 TGTTGATGCCACAACTCTCAGGAAATACGAAATGGATTCTGACATACGGGCGT 200

RESULT 9
 ADR24325
 ID ADR24325 standard; DNA; 926 BP.
 XX
 AC ADR24325;
 XX DT 21-OCT-2004 (first entry)
 XX DE Breast cancer prognosis marker #186.
 XX KW ds; breast cancer; prognosis; gene expression; diagnosis.
 XX OS Homo sapiens.
 XX PN WO2004065545-A2.
 XX PD 05-AUG-2004.
 XX PR 15-JAN-2004; 2004WO-US001100.
 XX PR 15-JAN-2003; 2003US-00342887.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 XX PT Classifying a breast cancer patient according to prognosis comprises
 PT determining the similarity between the level of expression of each of
 PT five genes in a cell sample taken from patient, to control levels.
 XX PS Disclosure; SEQ ID NO 186; 226pp; English.
 XX The invention relates to a method of classifying a breast cancer patient
 CC according to prognosis by determining the similarity between the level of
 CC expression of each of five genes for which markers are listed in the
 CC specification, in a cell sample taken from the breast cancer patient, to
 CC control levels of expression for each respective five genes to obtain a
 CC patient similarity value. The methods are useful for classifying a breast
 CC cancer patient according to prognosis. Kits and computer program products
 CC are useful for data analysis using the diagnostic, prognostic and
 CC statistical methods of the invention. This sequence corresponds to a
 CC marker used in the method of the invention.
 XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.17e-86 Length: 926
 Score: 753.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 13 Indels: 0
 DB: Gaps: 0
 US-10-789-251-26 (1-144) x ADR24325 (1-926)
 QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgIleSer 20
 QY 141 TGTTGATGCCACAACTCTCAGGAAATACGAAATGGATTCTGACATACGGGCGT 200

QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgLeuArgArgThrGluSerLeuGln 40
 DR DR WPI: 2004-667683/65.
 Db 201 GTCGAAGCCAAAGATGGAACTGACATCAGATCTAGGGAGCTGATCTGCAA 260
 PR P-PSDB; ADS18363, ADS18373.
 QY 41 AspThrIysProAlaAsnArgCysCysLeuArgIleLeuArgLeuLeuAsp 60
 PT New antibody that selectively binds to a Zcyto10 polypeptide useful for
 Db 261 GACACAAAGCTCTGGAAATGATGCTGCTCTGGCCATTCTGAC 320
 PR modulating cell proliferation, cell differentiation or cytokine
 production in the prevention or treatment of e.g. autoimmune diseases,
 cancer or wounds.
 QY 61 ArgValPhelYlsnTyrGlnIhrProAspHsTyrThrLeuArgLeuLeuAsp 80
 PT disclosure; SEQ ID NO 1; 31pp; English.
 Db 321 AGGGATTTAAACATCCAGCCCTGACCATTAATCTCCGGAGATAGCAGCTC 380
 PR XX
 CC The present invention relates to a mammalian cytokine-like polypeptide,
 CC Zcyto10 and its encoding Polynucleotide. The invention is useful for
 CC modulating cell proliferation, cell differentiation or cytokine
 CC production in the prevention or treatment of conditions such as
 CC autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid
 CC arthritis, asthma or psoriasis) and cancer or wounds. The invention is
 CC also useful in gene therapy. The present sequence is the human Zcyto10
 CC protein encoding DNA. This Zcyto10 gene is located on chromosome 1q32.2.
 XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
 QY 141 GluGluLysIleGlu 144
 Db 561 GAGGAGACGAA 572
 RESULT 10
 ADS18362
 ID ADS18362 standard; DNA; 926 BP.
 AC
 XX
 AC ADS18362;
 DT 02-DEC-2004 (first entry)
 XX Human Zcyto10 protein encoding DNA #1.
 DE
 KW Zcyto10; cytokine-like polypeptide; cell proliferation;
 KW cell differentiation; autoimmune disease; diabetes; multiple sclerosis;
 KW rheumatoid arthritis; asthma; psoriasis; cancer; wound; gene therapy;
 KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
 KW antiarthritic; antiasthmatic; antipsoriatic; cytostatic; vulnerary;
 KW human; gene; chromosome 1q32.2; dsb.
 OS Homo sapiens.
 XX
 PH Key location/Qualifiers
 FT CDS 45. .575
 FT /tag= b
 FT /product= "Zcyto10 protein"
 FT sig_peptide 45. .116
 FT /tag= a
 FT mat_peptide 117. .572
 FT /tag= c
 FT /product= "Mature zcyto10 protein"
 XX US2004181040-A1.
 PD 16-SEP-2004.
 XX
 PR 29-DEC-2003; 2003US-00748484.
 XX
 PR 26-NOV-1997; 97US-00666597P.
 PR 25-NOV-1998; 98US-00199586.
 PR 15-APR-2003; 2003US-00413661.
 PR (CONK/) CONKLIN D C.
 PA (HALD/) HALDEMAN B A.
 PA (GROS/) GROSSMANN A.
 XX
 PI Conklin DC, Haldeman BA, Grossmann A;

XX RESULT 11
 ID AEA50048
 PR XX AEA50048 standard; cDNA; 926 BP.
 AC AEA50048;
 XX
 DT 11-AUG-2005 (first entry)
 PR XX
 DE Full length IL-20 coding sequence.

XX
 KW ss; gene; Antiinflammatory; Gastrointestinal-Gen.; Antiulcer;
 KW Antiarthritic; Dermatological; Antipsoriatic; Antibacterial;
 KW Immunosuppressive; Antimicrobial; IL-Antagonist-20; interleukin-20;
 KW IL-20; inflammation; inflammatory bowel disease; ulcerative colitis;
 KW Crohns disease; arthritis; atopic dermatitis; psoriasis; endotoxemia;
 KW septicemia; toxic shock syndrome ; infectious disease.
 OS Homo sapiens.

XX
 Key Location/Qualifiers
 FT CDS 45. .575
 FT /tag= a
 XX WO2005052000-A2.
 XX 09-JUN-2005.
 XX 19-NOV-2004; 2004WO-US039071.
 XX 21-NOV-2003; 2003US-0524131P.
 XX 24-MAR-2004; 2004US-0555857P.
 PA (ZYMO) ZYMOGENETICS INC.
 XX Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekher YA;
 PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
 XX WPI; 2005-405359/41.
 DR P-PSDB; AEA50049, AEA50050.
 XX
 PT producing an antibody to an interleukin-20 (IL-20) polypeptide, useful
 PT for treating inflammatory diseases e.g., Crohn's disease, by inoculating
 PT an animal with the polypeptide eliciting an immune response to produce
 PT
 XX Example 1; SEQ ID NO 1; 260pp; English.
 XX
 CC This sequence encodes full length interleukin-20 (IL-20), longer form IL-
 20x1. The method of the invention for producing an antibody to IL-20
 CC comprises inoculating an animal with an IL-20 polypeptide which elicits
 CC an immune response in the animal to produce the antibody, and isolating
 CC the antibody from the animal. The antibody is useful for treating a
 CC pathological condition in a subject associated with IL-20 activity such
 CC as chronic inflammatory condition, specifically inflammatory bowel
 CC disease, ulcerative colitis, Crohns disease, arthritis, atopic
 CC dermatitis and psoriasis, or acute inflammatory condition such as
 CC endotoxemia, septicemia, toxic shock syndrome and infectious disease. An
 CC antagonist of IL-20 is useful for treating a mammal afflicted with an
 CC inflammatory disease in which IL-20 plays a role such that the
 CC antibody fragment, or binding polypeptide that specifically binds a
 CC polypeptide or polypeptide fragment of IL-20 or a polypeptide or
 CC 20-18 reduced. The method is useful for producing such therapeutic
 CC antibody or antibody fragment, produced using the above
 CC method, binds to IL-20, and inhibits or reduces the pro-inflammatory
 CC activity of IL-20. IL-20-induced proliferation or differentiation of
 CC hematopoietic cells and hematopoietic cell progenitors may be reduced or
 CC inhibited using the antibody.
 XX
 SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.17e-86 Length: 926
 Score: 755.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 14 Deletions: 0
 Gaps: 0
 US-10-789-251-26 (1-144) x AEA50048 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
 Db 141 TGTGTGATGCCAACACTTCGGAATAGAAATTCTGACATACGGCGAT 200
 QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleArgLeuArgThrGluSerLeuGln 40
 Db 201 GTGCAAGCCAGATGGACATGACTCAGATCTTAAAGGAGCTAGTCCTTGCA 260
 QY 41 AspThrLysProAlaAspArgCysCysteLeuArgIleArgLeuArgLeuTrpLeuSp 60
 Db 261 GACACAAAGCCTCGAATGATGCTGCTGCCCTCTGGCAATTCTGAGCTCTTGCA 320
 QY 61 ArgValPheLysAlaValArgIleProLysPheIleArgIleArgLeuArgLysIleSerSerIeu 80
 Db 321 AGGCTTAAACTACAGACGCCCTGACATTACTCTCGGAGATCACAGACAGTCGC 380
 QY 81 AlanSerPheLeuThrIleLysAspLeuArgLysCysBisAlaHisMethCys 100
 Db 381 GCCATTCCTTCCTTACATCAGAGACCTCGCGCTGCTGATGCCACATGACATGC 440
 QY 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysIeu 120
 Db 441 CATGTGGGGAGGAGCATGAGAAGAAATACAGCCAGATCTGAGTACTTGTGAAGCTG 500
 QY 121 GluProGlnAlaAlaValValValAlaLeuGlyGluIleAspIleLeuGlnTrpMet 140
 Db 501 GAACTCAAGCAGCAGTGTGAGGCTTGGGGAACTAGACATTCTCTGCATGGATG 560
 QY 141 GluGluThrGlu 144
 Db 561 GAGGGAGCAGAA 572

RESULT 12
 AEA28786 standard; cDNA; 926 BP.
 ID AEA28786
 XX AC AEA28786;
 XX DT 11-AUG-2005 (first entry)
 XX DE Human interleukin 20 (IL-20) precursor cDNA clone.
 XX
 KW antibody production; cytokine; antiinflammatory; Gastrointestinal-Gen.;
 KW antiulcer; antiarthritic; dermatological; antipsoriatic; antibacterial;
 KW immunosuppressive; antimicrobial; inflammation; inflammatory bowel disease; ulcerative colitis; Crohns disease;
 KW arthritis; atopic dermatitis; psoriasis; cancer; endotoxemia; sepsis; endotoxic shock; infectious disease; IL-20; interleukin-20; ss; gene.
 XX OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FT CDS 45. .575
 FT /tag= a
 /product= "Human interleukin 20 (IL-20) protein"
 XX WO2005052001-A2.
 XX 09-JUN-2005.
 XX
 PF 19-NOV-2004; 2004WO-US039097.
 XX
 PR 21-NOV-2003; 2003US-0524131P.
 PR 24-MAR-2004; 2004US-0555857P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Wu, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekher YA;
 PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
 XX WPI; 2005-405360/41.
 DR P-PSDB; AEA28787.
 XX

PT Producing an antibody to an interleukin 20RA (IL-20RA) polypeptide, PT useful for treating inflammatory diseases e.g., arthritis, by inoculating PT an animal with the polypeptide which elicits an immune response to PT produce the antibody.

PS Example 1; SEQ ID NO 1; 265pp; English.

XX The invention relates to a novel method for producing an antibody to a polypeptide. The method comprises inoculating an animal with a polypeptide selected from any of SEQ ID NO: 14, 15, 17 or 19 as given in the specification, where the polypeptide elicits an immune response in the animal to produce the antibody, and isolating the antibody from the animal. The antibody specifically binds to the pro-inflammatory cytokine interleukin 20 (IL-20 or ZcytP) or one its receptors IL-20RA (ZcytP^{R7}) or IL-20RB (PDIR81). The method of the invention demonstrates antiinflammatory, gastrointestinal, antiborotic, antivincer, antiarthritic, dermatological, antiseptemic, antibacterial, immunosuppressive and antimicrobial applications. The antibody may be useful for treating a pathological condition in a subject associated with IL-20RA, such as a chronic inflammatory condition selected from inflammatory bowel disease, ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis and psoriasis, cancer, or an acute inflammatory condition such as endotoxemia, septicemia, toxic shock syndrome and infectious disease. The current sequence is that of a human IL-20 precursor cDNA clone of the CC invention.

XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

SQ Alignment Scores:

Score: 1.17e-86

Length: 926

Matches: 144

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 1 CyvalleAlaThrAsnLeuGluLeuArgAspGlyPheSerAspIleArgGlySer 20

Db 141 TGTGTGATGCCACAACCTCAGGAAATAGAATGGATTCTGACATCGGGCGT 200

Query Match: 100.00%

DB: 14

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 1 CyvalleAlaThrAsnLeuGluLeuArgAspGlyPheSerAspIleArgGlySer 20

Db 21 ValGlnAlaValAspGlyAsnLeuAspIleArgIleLeuArgArgThrGlySerLeuGln 40

Query Match: 100.00%

DB: 201 GTCGAGCAGATGGAACATGACTCAGATCTAGAGGAGCTGAGCTTCAA 260

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 41 AspThrLysProAlaAsnArgCysCysLeuLeuLeuLeuArgIleGlySerLeuAsp 60

Db 261 GACACAGGCTCGCGAACTGATGCTCCCTCGCCATTGTGAGCTACATCGAC 320

Query Match: 100.00%

DB: 61 ArgValPheLysSerArgLysProAspPheSerAspIleArgIleLeuArgSerLeu 80

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 321 AGGGATTAAACTACCAAGACCCCTGACCATATACTCTCCGGAGATCAGCAGCTC 380

Query Match: 99.31%

DB: 81 AlaAsnSerPheLeuThrIleAlaValAspLeuGluCysHisAlaIleMetThrCys 100

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 381 GCGATTCCTCTTACCATCAGAAGCAGCTCGCTGATGCCACATGACATGC 440

Query Match: 99.47%

DB: 82 TGTGTGATGCCACAACCTCAGGAAATAGAATGGATTCTGACATCGGGCGT 500

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 101 HisCysGlyGluIleAlaMetLysIleSerGlySerGlySerAspIleArgIleLeu 120

Db 441 CATGTGTCGGAGGAGCAGTGGAAATACGCCAGATCTGAGTCACTTGAGCTG 500

Query Match: 99.31%

DB: 121 GluProGlnAlaIleAlaValAspLeuGlyGluLeuAspIleLeuLeuGlnProMet 140

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 501 GAACTCTAGGAGCAGTGTGAAGGCTTGGGGAACTAGACATCTCTGCAATGGATG 560

Query Match: 99.31%

DB: 141 GluGluLysGlu 144

US-10-789-251-26 (1-144) x AEA28786 (1-926)

Qy 561 GAGGAGAGAGAA 572

Query Match: 99.31%

DB: ABV75151

RESULT 13

ID ABV75151 standard; DNA: 462 BP.

XX ABV75151; AC XX DT 19-FEB-2003 (first entry) XX DB Human interleukin-20 (IL-20) codon optimised fragment zcyt010X1. XX KW Protein synthesis; data mining; recombinant; interleukin-20; IL-20; XX human; ds. XX OS Homo sapiens. XX PN WO200283853-A2. XX PR 13-APR-2001; 2001US-0283688P. XX PA (ZYMO) ZYMOGENETICS INC. XX PI Powder TA, Chan C; XX DR WPI; 2003-067576/06. XX PT New polynucleotide, useful for producing a nucleic acid construct for PT expression of an amino acid sequence of interest. XX PS Example 1; Page 36; 40pp; English.

XX The invention provides a new purified polynucleotide that comprises the nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide sequence of 13 nucleic acids, where the sequence has homology with 13 base pair (bp) sequence, where at least 5 nucleic acids are identical to a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16 or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected from 9 sequences (ABV75144-150) where at least 50% nucleotides are either adenine or thymine, and where only B encodes a stop codon. The polynucleotide is useful for producing a nucleic acid construct for expression of an amino acid sequence of interest. The present sequence represents a human interleukin-20 (IL-20) codon optimised fragment for expression in E. coli

XX Sequence 462 BP; 121 A; 131 C; 117 G; 93 T; 0 U; 0 Other;

SQ Alignment Scores:

Score: 1.38e-86

Length: 462

Matches: 143

Conservative: 1

Mismatches: 0

Indels: 0

Gaps: 0

US-10-789-251-26 (1-144) x ABV75151 (1-462)

Qy 1 CyvalleAlaThrAsnLeuGlnGluIleArgAspGlyPheSerAspIleArgGlySer 20

Db 28 TGTGTGATGCCACAACCTCAGGAAATACTGAGTCACTTGAGCTGAGCTG 87

Query Match: 99.31%

DB: 21 ValGlnAlaValAspGlyAsnLeuAspIleArgIleLeuArgArgThrGlySerLeu 40

US-10-789-251-26 (1-144) x ABV75151 (1-462)

Qy 88 GTCGAGCAGATGCTAACATGACATCTGAGTCACTTGAGCTGAGCTG 147

Query Match: 99.31%

DB: 41 AspThrLysProAlaAsnArgCysCysLeuLeuLeuLeuArgIleGlySerLeu 60

US-10-789-251-26 (1-144) x ABV75151 (1-462)

Qy 148 GACCAACCGCGAACCGTGTCTGCTGCGCACCTCTGCGCTGATCTG 207

Query Match: 99.31%

DB: 61 ArgValPheLysSerArgLysProAspPheSerAspIleArgIleLeuArgSerLeu 80

US-10-789-251-26 (1-144) x ABV75151 (1-462)

Qy 208 CGGTTCAAACTACAGACCCGACCACTATCCCGTAAATCAGCAGCTG 267

Query Match: 99.31%

DB: ABV75151

XX
 CC The invention provides a new purified polynucleotide that comprises the
 CC nucleic acid sequence A-B-C-D-E, where: A= start codon, B= polynucleotide
 CC sequence of 13 nucleic acids, where the sequence has homology with 13
 CC base pair (bp) sequence, where at least 5 nucleic acids are identical to
 CC a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
 CC code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16
 CC or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide
 CC sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected
 CC from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
 CC adenine or thymine, and where only E encodes a stop codon. The
 CC polynucleotide is useful for producing a nucleic acid construct for
 CC expression of an amino acid sequence of interest. The present sequence
 CC represents a sequence comprising an expression cassette (EC)
 CC polynucleotide sequence inserted upstream of a human interleukin-20 (IL-
 CC 20) codon optimised fragment for expression in E. coli
 XX

Sequence 513 BP; 143 A; 145 C; 126 G; 99 T; 0 U; 0 Other;

Alignment Scores:
 pred. No.: 1.61e-86 Length: 513
 Score: 749.00 Matches: 143
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.31% Mismatches: 0
 Query Match: 99.47% Indels: 0
 DB: 8 Gaps: 0

US-10-789-251-26 (1-144) x ABV75154 (1-513)

QY 1 CysvalleAlaThrAspLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
 Db 79 TGTCTGATGCCACCAACTCTGAGAAATCGTACGGTTCTCTGAGATCCGTGGAGC 138
 QY 21 ValGlnAlaLysAspGlyIleAspLeuGlyAspIleLeuGlyIleAspLeuGlyIleAsp 40
 Db 139 GTCGAGGCCAAAGTGTCACATGACTCGATCCGATCTGGCTGGCTGGTACCGAGCTCGAG 198
 QY 41 AspThrLysProAlaAspArgCysCysLeuLeuArgIleLeuLeuArgLeuTyroLeuAsp 60
 Db 199 GACACCAACGGGGAAACGGGTTGCTGCTGGCCACCTGGCTGCTGCTGCTGCTGCTGGAC 258
 QY 61 ArgValPhelAsnTyrGlnIleProAspHisTyrIleLeuIleArgValLeuSerIle 80
 Db 259 CGTCTTTCAAAACTACCAAGACCCGGACACTATACCTTGCTAAATCAGCAGCTG 318
 QY 81 AlaAsnSerPhelAsnThrIleIleLysAspLeuLeuArgLeuCysIleAlaHisMetThrCys 100
 Db 319 GCGAACTCCTTCCTGACCCATCAAAACGACCGCTCGCTGTCAGGCCAACGACCTG 378
 QY 101 HisCysGlyGlyIleGluIleAlaMetLysTyrSerGlnIleLeuSerHisPheGluIleLeu 120
 Db 379 CACTGGTGGAGGAAGCAGTGAAGAAATTCAGCCAGATTCCTGACCTTCGAAACTG 438
 QY 121 GluProGlnAlaAlaAlaValValValLeuAspIleLeuLeuGlnTrpMet 140
 Db 439 GAACCGCAGGAGCAGCTGGGAAGCTCTGGTGAACCTGACAGCAATCTGCTGAGTGGATG 498
 QY 141 GluGluThrGlu 144
 Db 499 GAGGAGACGAA 510

Search completed: December 28, 2005, 11:56:33
 Job time : 505 sec8